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Amplified Genes Involved in Cancer

This application claims priority to U. S. Serial No. 60/427,202, filed November 19, 2002, and U. S. Serial No. 60/434,434, filed December 19, 2002, the entireties of which are hereby incorporated by reference.

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BACKGROUND OF THE INVENTION

1. Field of the Invention

The invention relates to oncogenes and to cancer diagnostics and therapeutics. More specifically, the present invention relates to amplified and/or overexpressed SPHK1, EDG4, 15 EDG5, and EDG8 genes, which are involved in certain types of cancers. The invention pertains to the amplified genes, their encoded proteins, and antibodies, inhibitors, activators and the like and their use in cancer diagnostics, vaccines, and anti-cancer therapy, including colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, or bladder cancer.

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2. Background of the Invention

Cancer and Gene Amplification:

Cancer is the second leading cause of death in the United States, after heart disease (Boring, *et al.*, *CA Cancer J. Clin.*, 43:7, 1993), and it develops in one in three Americans. One 25 of every four Americans dies of cancer. Cancer features uncontrolled cellular growth, which

results either in local invasion of normal tissue or systemic spread of the abnormal growth. A particular type of cancer or a particular stage of cancer development may involve both elements.

The division or growth of cells in various tissues functioning in a living body normally takes place in an orderly and controlled manner. This is enabled by a delicate growth control mechanism, which involves, among other things, contact, signaling, and other communication between neighboring cells. Growth signals, stimulatory or inhibitory, are routinely exchanged between cells in a functioning tissue. Cells normally do not divide in the absence of stimulatory signals, and will cease dividing when dominated by inhibitory signals. However, such signaling or communication becomes defective or completely breaks down in cancer cells. As a result, the cells continue to divide; they invade adjacent structures, break away from the original tumor mass, and establish new growth in other parts of the body. The latter progression to malignancy is referred to as "metastasis."

Cancer generally refers to malignant tumors, rather than benign tumors. Benign tumor cells are similar to normal, surrounding cells. These types of tumors are almost always encapsulated in a fibrous capsule and do not have the potential to metastasize to other parts of the body. These tumors affect local organs but do not destroy them; they usually remain small without producing symptoms for many years. Treatment becomes necessary only when the tumors grow large enough to interfere with other organs. Malignant tumors, by contrast, grow faster than benign tumors, and they penetrate and destroy local tissues. Some malignant tumors may spread throughout the body via blood or the lymphatic system. The unpredictable and uncontrolled growth makes malignant cancers dangerous, and fatal in many cases. These tumors are not morphologically typical of the original tissue and are not encapsulated. Malignant tumors commonly recur after surgical removal.

Accordingly, treatment ordinarily is directed towards malignant cancers or malignant tumors. The intervention of malignant growth is most effective at the early stage of the cancer development. Thus, it can be important to discover sensitive markers for early signs of cancer formation and to identify potent growth suppression agents associated therewith. The development of such diagnostic and therapeutic agents involves an understanding of the genetic

control mechanisms for cell division and differentiation, particularly in connection with tumorigenesis.

Cancer can be caused by inherited or acquired mutations in cancer genes, which have normal cellular functions and which induce or otherwise contribute to cancer once mutated or
5 expressed at an abnormal level. Certain well-studied tumors carry several different independently mutated genes, including activated oncogenes and inactivated tumor suppressor genes. Each of these mutations appears to be responsible for imparting some of the traits that, in aggregate, represent the full neoplastic phenotype (Land *et al.*, *Science*, 222:771, 1983; Ruley, *Nature*, 4:602, 1983; Hunter, *Cell*, 64:249, 1991).

10 One such mutation is gene amplification. Gene amplification involves a chromosomal region bearing specific genes undergoing a relative increase in DNA copy number, thereby increasing the copies of any genes that are present. In general, gene amplification often results in increased levels of transcription and translation, producing higher amounts of the corresponding gene mRNA and protein. Amplification of genes can cause deleterious effects, which contribute
15 to cancer formation and proliferation (Lengauer *et al.* *Nature*, 396:643-649, 1999).

It is commonly appreciated by cancer researchers that whole collections of genes are demonstrably overexpressed or differentially expressed in a variety of different types of tumor cells. Yet, often only a very small number of these overexpressed genes are likely to be causally
20 involved in the cancer phenotype. The remaining overexpressed genes likely are secondary consequences of more basic primary events, for example, overexpression of a cluster of genes, involved in DNA replication. Nevertheless, gene amplification is established as an important genetic alteration in solid tumors (Knuutila *et al.*, *Am. J. Pathol.*, 152(5):1107-23, 1998; Knuutila *et al.*, *Cancer Genet. Cytogenet.*, 100(1):25-30, 1998).

The overexpression of certain well known genes, for example, *c-myc*, has been observed
25 at fairly high levels in the absence of gene amplification (Yoshimoto *et al.*, *JPN J. Cancer Res.*, 77(6):540-5, 1986), although these genes are frequently amplified (Knuutila *et al.*, *Am. J. Pathol.*, 152(5):1107-23, 1998) and thereby activated. Such a characteristic is considered a hallmark of oncogenes. Overexpression in the absence of amplification may be caused by higher

transcription efficiency in those situations. In the case of *c-myc*, for example, Yoshimoto *et al.* showed that its transcriptional rate was greatly increased in the tested tumor cell lines. The characteristics and interplay of overexpression and amplification of a gene in cancer tissues, therefore, provide significant indications of the gene's role in cancer development. That is, increased DNA copies of certain genes in tumors, along with and beyond their overexpression, may point to their functions in tumor formation and progression.

It must be remembered that overexpression and amplification are not the same phenomenon. Overexpression can be obtained from a single, unamplified gene, and an amplified gene does not always lead to greater expression levels of mRNA and protein. Thus, it is not possible to predict whether one phenomenon will result in, or is related to, the other. However, in situations where both amplification of a gene and overexpression of the gene product occur in cells or tissues that are in a precancerous or cancerous state, then that gene and its product present both a diagnostic target and a therapeutic opportunity for intervention. Amplification, without overexpression, and overexpression, without amplification, also can be correlated with and indicative of cancers and pre-cancers.

Because some genes are sometimes amplified as a consequence of their location next to a true oncogene, it is also beneficial to determine the DNA copy number of nearby genes in a panel of tumors so that amplified genes that are in the epicenter of the amplification unit can be distinguished from amplified genes that are occasionally amplified due to their proximity to another, more relevant, amplified gene.

Thus, discovery and characterization of amplified cancer genes, along with and in addition to their features of overexpression or differential expression, will be a promising avenue that leads to novel targets for diagnostic, vaccines, and therapeutic applications.

Additionally, the completion of the working drafts of the human genome and the paralleled advances in genomics technologies offer new promises in the identification of effective cancer markers and the anti-cancer agents. The high-throughput microarray detection and screening technology, computer-empowered genetics and genomics analysis tools, and multi-platform functional genomics and proteomics validation systems, all assist in applications

in cancer research and findings. With the advent of modern sequencing technologies and genomic analyses, many unknown genes and genes with unknown or partially known functions can be revealed.

Genomic amplification and overexpression of SPHK1, EDG4, EDG5, and EDG8 genes
5 and their role in tumorigenesis were not known until the instant invention. In addition to antibodies that bind tumor cells expressing SPHK1, EDG4, EDG5, or EDG8, the possibility to treat tumors with antibodies that block the oncogenic function of SPHK1, EDG4, EDG5, or EDG8, and thereby mediate tumor-cell killing, also were not known until the present invention.

Therefore, there is a need in the art for an understanding of SPHK1, EDG4, EDG5 and
10 EDG8 genes regulation. Understanding the physiological role of human SPHK1, EDG4, EDG5, and EDG8 genes will facilitate early diagnosis of abnormalities associated therewith and lead to appropriate therapies to treat such abnormalities. These needs are satisfied for the first time by the present invention.

15 **SUMMARY OF THE INVENTION**

The present invention relates to isolation, characterization, overexpression and implication of genes, including amplified genes, in cancers, methods and compositions for use in diagnosis, vaccines, prevention and treatment of tumors and cancers, for example, colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and
20 neck cancer, stomach cancer, esophagus cancer, or bladder cancer, in mammals, for example, humans. The invention is based on the finding of novel attributes of SPHK1, EDG4, EDG5, and EDG8. Specifically, amplification and/or overexpression of SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 genes in tumors, including lung tumors, breast tumors, colon tumors, ovarian tumors, brain tumors, liver tumors, kidney tumors, head and neck tumors, stomach tumors,
25 esophagus tumors, and bladder tumors and their role in oncogenesis was not known until the instant invention.

These novel attributes include the overexpression of the SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 genes in certain cancers, for example, colon cancer and/or ovarian cancer and/or brain cancer and/or breast cancer and/or lung cancer, and/or liver, and/or kidney, and/or bladder, and the frequent amplification of SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 in cancer cells. The SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 genes and their expressed protein products can thus be used diagnostically or as targets for cancer therapy; and they also can be used to identify and design compounds useful in the diagnosis, prevention, and therapy of tumors and cancers.

Until the present invention, certain utilities of the SPHK1, EDG4, EDG5 and EDG8 genes associated with diagnostics and therapeutics in various cancers were not known. Moreover, until the present invention, SPHK1, EDG4, EDG5, and EDG8 genes have not been fully characterized to allow their role in tumor development to be completely understood.

According to one aspect of the present invention, the use of SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 in gene therapy, development of small molecule inhibitors, small interfering RNAs (siRNAs), microRNAs (miRNAs), and antisense nucleic acids, and development of immunodiagnostics and immunotherapies, are provided. The present invention includes production and the use of antibodies, for example, monoclonal, polyclonal, single-chain and engineered antibodies (including humanized antibodies) and fragments, which specifically bind SPHK1, EDG4, EDG5, or EDG8 proteins and polypeptides. The invention also includes antagonists and inhibitors of SPHK1, EDG4, EDG5, and EDG8 proteins that can inhibit one or more of the functions or activities of SPHK1, EDG4, EDG5, or EDG8, respectively. Suitable antagonists can include small molecules (molecular weight below about 500 Daltons), large molecules (molecular weight above about 500 Daltons), and antibodies (including fragments and single chain antibodies) that bind and interfere or neutralize SPHK1, EDG4, EDG5, or EDG8 proteins, polypeptides which compete with a native form of SPHK1, EDG4, EDG5, or EDG8 proteins for binding to a protein that naturally interacts with SPHK1, EDG4, EDG5, or EDG8 proteins, and nucleic acid molecules that interfere with transcription and/or translation of the SPHK1, EDG4, EDG5, or EDG8 gene (for example, antisense nucleic acid molecules, triple

helix forming molecules, ribozymes, microRNAs, and small interfering RNAs), respectively. The present invention also includes useful compounds that influence or attenuate activities of SPHK1, EDG4, EDG5, or EDG8.

In addition, the present invention provides inhibitors of SPHK1, EDG4, EDG5, or EDG8 activity, such as antibodies, that block the oncogenic function or anti-apoptotic activity of SPHK1, EDG4, EDG5, or EDG8, respectively.

Other inhibitors include antibodies that bind to a cell over-expressing SPHK1, EDG4, EDG5, or EDG8 protein, thereby resulting in suppression or death of the cell.

The present invention further provides molecules that can decrease the expression of SPHK1, EDG4, EDG5, or EDG8 by affecting transcription or translation. Small molecules (molecular weight below about 500 Daltons), large molecules (molecular weight above about 500 Daltons), and nucleic acid molecules, for example, ribozymes, miRNAs, siRNAs and antisense molecules, including antisense RNA, antisense DNA or decoy molecules (for example, Morishita *et al.*, *Ann. N Y Acad. Sci.*, 947:294-301, 2001; Andratschke *et al.*, *Anticancer Res.*, 21:(5)3541-3550, 2001), may all be utilized to inhibit the expression or amplification.

As mentioned above, the SPHK1, EDG4, EDG5, and EDG8 gene sequences also can be employed in an RNA interference context. The phenomenon of RNA interference is described and discussed in Bass, *Nature*, 411: 428-29 (2001); Elbashir *et al.*, *Nature*, 411: 494-98 (2001); and Fire *et al.*, *Nature*, 391: 806-11 (1998), where methods of making interfering RNA also are discussed.

In one aspect, the present invention provides methods for diagnosing a cancer (diagnostics uses) for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a mammal, which comprises, in any practical order, obtaining a test sample from a region in the tissue that is suspected to be precancerous or cancerous; and comparing the number of SPHK1, EDG4, EDG5, or EDG8 gene copies measured (for example, quantitatively and/or qualitatively) in the sample to a control sample or a known

value, thereby determining whether the SPHK1, EDG4, EDG5, or EDG8 gene is amplified in the test sample, respectively, wherein amplification of the SPHK1, EDG4, EDG5, or EDG8 gene indicates a cancer or a precancerous condition in the tissue.

5 In another aspect, the present invention provides methods for diagnosing a cancer (diagnostics uses) for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a mammal, which comprises, in any practical order, obtaining a test sample from a region in the tissue that is suspected to be precancerous or cancerous; obtaining a control sample from a region in the tissue or other tissues that are normal;
10 and detecting or measuring in both the test sample and the control sample the level of SPHK1, EDG4, EDG5, or EDG8 mRNA transcripts, wherein a level of the transcripts higher in the test sample than that in the control sample indicates a cancer or a precancerous condition in the tissue. In another aspect the control sample may be obtained from a different individual or be a normalized value based on baseline data obtained from a population.

15 In another aspect, the present invention provides methods for diagnosing a cancer (diagnostics uses) for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a mammal, which comprises, in any practical order, obtaining a test sample from a region in the tissue that is suspected to be precancerous or cancerous; and comparing the number of SPHK1, EDG4, EDG5, or EDG8 DNA copies detected
20 (for example, quantitatively and/or qualitatively) in the sample to a control sample or a known value, thereby determining whether the SPHK1, EDG4, EDG5, or EDG8 gene is amplified in the test sample, respectively, wherein amplification of the SPHK1, EDG4, EDG5, or EDG8 gene indicates a cancer or a precancerous condition in the tissue.

25 Another aspect of the present invention provides methods for diagnosing a cancer (diagnostics uses) for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a mammal, which comprises, in any practical order,

obtaining a test sample from a region in the tissue that is suspected to be precancerous or cancerous; contacting the sample with anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 antibodies, and detecting in the test sample, the level of SPHK1, EDG4, EDG5, or EDG8 expression, respectively, wherein an increased level of the SPHK1, EDG4, EDG5, or EDG8 expression in the test sample, as compared to a control sample or a known value indicates a precancerous or a cancerous condition in the tissue. In another aspect, the control sample may be obtained from a different individual or be a normalized value based on baseline data obtained from a population. Alternatively, a given level of SPHK1, EDG4, EDG5, or EDG8, representative of the cancer-free population, that has been previously established based on measurements from normal, cancer-free animals, can be used as a control. A control data point from a reference database, based on data obtained from control samples representative of a cancer-free population, also can be used as a control.

In another aspect, the present invention relates to methods for comparing and compiling data wherein the data is stored in electronic or paper format. Electronic format can be selected from the group consisting of electronic mail, disk, compact disk (CD), digital versatile disk (DVD), memory card, memory chip, ROM or RAM, magnetic optical disk, tape, video, video clip, microfilm, internet, shared network, shared server and the like; wherein data is displayed, transmitted or analyzed via electronic transmission, video display, telecommunication, or by using any of the above stored formats; wherein data is compared and compiled at the site of sampling specimens or at a location where the data is transported following a process as described above.

In another aspect, the present invention provides methods for preventing, controlling, reversing, or suppressing cancer growth (and analogous uses) in a mammalian organ and tissue, for example, in the colon, ovary, brain, breast, lung, liver, kidney, head and neck, stomach, esophagus, or bladder, which comprises administering an inhibitor of SPHK1, EDG4, EDG5, or EDG8 protein to the organ or tissue, thereby inhibiting SPHK1, EDG4, EDG5, or EDG8 protein activities, respectively. Such inhibitors may be, among other things, an antibody to SPHK1,

EDG4, EDG5, or EDG8 protein or polypeptide portions thereof, an antagonist to SPHK1, EDG4, EDG5, or EDG8 protein, respectively, or other small or large molecules.

In a further aspect, the present invention provides a method for preventing, controlling, reversing, or suppressing cancer growth (and analogous uses) in a mammalian organ and tissue, for example, in the colon, ovary, brain, breast, lung, liver, kidney, head and neck, stomach, esophagus, or bladder, which comprises administering to the organ or tissue a nucleotide molecule that is capable of interacting with SPHK1, EDG4, EDG5, or EDG8 DNA and/or RNA and thereby blocking or interfering the SPHK1, EDG4, EDG5, or EDG8 gene functions, respectively. Such nucleotide molecules can be an antisense nucleotide of the SPHK1, EDG4, EDG5, or EDG8 gene, a ribozyme of SPHK1, EDG4, EDG5, or EDG8 RNA, a small interfering RNA (siRNA) or it may be a molecule capable of forming a triple helix with the SPHK1, EDG4, EDG5, or EDG8 gene, respectively.

In a further aspect, the present invention provides methods for preventing, controlling, reversing, or suppressing cancer growth (and analogous uses) in a mammalian organ and tissue, for example, in the colon, ovary, brain, breast, lung, liver, kidney, head and neck, stomach, esophagus, or bladder, which comprises administering to the organ or tissue a nucleotide molecule that is capable of interacting with SPHK1, EDG4, EDG5, or EDG8 DNA and/or RNA and thereby blocking or interfering the SPHK1, EDG4, EDG5, or EDG8 gene functions, respectively. Such nucleotide molecules can be an antisense nucleotide of the SPHK1, EDG4, EDG5, or EDG8 gene, a ribozyme of SPHK1, EDG4, EDG5, or EDG8 RNA; a small interfering RNA; a microRNA (miRNA); or it may be a molecule capable of forming a triple helix with the SPHK1, EDG4, EDG5, or EDG8 gene, respectively.

In still a further aspect, the present invention provides methods for determining the efficacy of a therapeutic treatment regimen for treating a cancer (and analogous uses), for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, for example, in a clinical trial or other research studies, which comprises, in any practical order, obtaining a first sample from the patient to ultimately obtain a

pre-treatment level; administering the treatment regimen to the patient; obtaining a second sample from the patient after a time period to ultimately obtain a test level; and detecting in both the first and the second samples the level of SPHK1, EDG4, EDG5, or EDG8 mRNA transcripts, wherein a level of the transcripts lower in the second sample (test level) than that in the first sample (pre-treatment level) indicates that the treatment regimen is effective in the patient.

In another aspect, the present invention provides methods for determining the efficacy of a compound to suppress a cancer (and analogous uses), for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, for example, in a clinical trial or other research studies, which comprises, in any practical order, obtaining a first sample from the patient to ultimately obtain a pre-treatment level; administering the treatment regimen to the patient; obtaining the second sample from the patient after a time period to ultimately obtain a test level; and detecting in both the first and the second samples the level of SPHK1, EDG4, EDG5, or EDG8 mRNA transcripts, wherein a level of the transcripts lower in the second sample (test level) than that in the first sample (pre-treatment level) indicates that the compound is effective to suppress such a cancer or a precancerous condition.

In another aspect, the present invention provides methods for determining the efficacy of a therapeutic treatment regimen for treating a cancer (and analogous uses), for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, for example, in a clinical trial or other research studies, which comprises, in any practical order, obtaining a first sample from the patient to ultimately obtain a pre-treatment level; administering the treatment regimen to the patient; obtaining a second sample from the patient after a time period to ultimately obtain a test level; and detecting in both the first and the second samples the number of SPHK1, EDG4, EDG5, or EDG8 DNA copies per cell, for example, thereby determining the overall or average SPHK1, EDG4, EDG5, or EDG8 gene amplification state in the first and second samples, respectively, wherein a lower number of SPHK1, EDG4,

EDG5, or EDG8 DNA copies per cell, for example, in the second sample (test level) than that in the first sample (pre-treatment level) indicates that the treatment regimen is effective.

In yet another aspect, the present invention provides methods for determining the efficacy of a therapeutic treatment regimen for treating a cancer (and analogous uses), for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, which comprises, in any practical order, obtaining a first sample from the patient to ultimately obtain a pre-treatment level; administering the treatment regimen to the patient; obtaining a second sample from the patient after a time period to ultimately obtain a test level; contacting the samples with anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 antibodies, and detecting the level of SPHK1, EDG4, EDG5, or EDG8 expression in both the first and the second samples, respectively. A lower level of the SPHK1, EDG4, EDG5, or EDG8 expression in the second sample (test level) than that in the first sample (pre-treatment level) indicates that the treatment regimen is effective in the patient.

Yet, in another aspect, the invention provides methods for determining the efficacy of a therapeutic treatment regimen for treating a cancer (and analogous uses), for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, comprising, in any practical order, the steps of: obtaining a first sample from the patient to ultimately obtain a pre-treatment level; administering the treatment regimen to the patient; obtaining a second sample from the patient after a time period to ultimately obtain a test level; contacting the samples with anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 antibodies, determining the expression level of SPHK1, EDG4, EDG5, or EDG8, in both the first and the second samples, by determining the overall expression divided by the number of cells present in each sample; and comparing the expression level of SPHK1, EDG4, EDG5, or EDG8 in the first and the second samples, respectively. A lower level of the SPHK1, EDG4, EDG5, or EDG8 expression in the second sample (test level) than that in the first sample (pre-treatment level)

indicates that the treatment regimen is effective in the patient, wherein the expression level is determined via a binding assay or other appropriate assay.

In still another aspect, the present invention provides methods for determining the efficacy of a compound to suppress a cancer (and analogous uses), for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, for example, in a clinical trial or other research studies, which comprises, in any practical order, obtaining a first sample from the patient to ultimately obtain a pre-treatment level; administering the treatment regimen to the patient; obtaining a second sample from the patient after a time period to ultimately obtain a test level; and detecting in both the first and the second samples the number of SPHK1, EDG4, EDG5, or EDG8 DNA copies per cell, for example, thereby determining the SPHK1, EDG4, EDG5, or EDG8 gene amplification state in the first and second samples, respectively, wherein a lower number of SPHK1, EDG4, EDG5, or EDG8 DNA copies per cell, for example, in the second sample (test level) than that in the first sample (pre-treatment level) indicates that the compound is effective.

In another aspect, the present invention provides methods for monitoring the efficacy of a therapeutic treatment regimen for treating a cancer (and analogous uses), for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, for example, in a clinical trial or other research studies, which comprises, in any practical order, obtaining a first sample from the patient to ultimately obtain a pre-treatment level; administering the treatment regimen to the patient; obtaining a second sample from the patient after a time period to ultimately obtain a test level; and detecting in both the first and the second samples the level of SPHK1, EDG4, EDG5, or EDG8 mRNA transcripts, wherein a level of the transcripts lower in the second sample (test level) than that in the first sample (pre-treatment level) indicates that the treatment regimen is effective in the patient.

Yet, in another aspect, the invention provides methods for monitoring the efficacy of a therapeutic treatment regimen for treating a cancer (and analogous uses), for example, a colon

cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, for example, in a clinical trial or sample from the patient to ultimately obtain a pre-treatment level; administering the treatment regimen to the patient; obtaining a second sample
5 from the patient after a time period to ultimately obtain a test level; determining in both the first and the second samples the level of SPHK1, EDG4, EDG5, or EDG8 mRNA transcripts, by determining the overall level divided by the number of cells present in each sample; and comparing the level of SPHK1, EDG4, EDG5, or EDG8 in the first and the second samples, respectively. A lower level of the SPHK1, EDG4, EDG5, or EDG8 mRNA transcripts in the
10 second sample (test level) than that in the first sample (pre-treatment level) indicates that the treatment regimen is effective in the patient, wherein the level can be determined via a binding assay or other appropriate assay.

In another aspect, the present invention provides methods for monitoring the efficacy of a compound to suppress a cancer (and analogous uses), for example, a colon cancer, an ovarian
15 cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, for example, in a clinical trial or other research studies, which comprises, in any practical order, obtaining a first sample from the patient to ultimately obtain a pre-treatment level; administering the treatment regimen to the patient; obtaining the second sample from the patient after a time
20 period to ultimately obtain a test level; and detecting in both the first and the second samples the level of SPHK1, EDG4, EDG5, or EDG8 mRNA transcripts, wherein a level of the transcripts lower in the second sample (test level) than that in the first sample (pre-treatment level) indicates that the compound is effective to suppress such a cancer or a precancerous condition.

In another aspect, the present invention provides methods for monitoring the efficacy of a
25 therapeutic treatment regimen for treating a cancer (and analogous uses), for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, for example, in a clinical trial or other research studies, which comprises, in any practical

order, obtaining a first sample from the patient to ultimately obtain a pre-treatment level; administering the treatment regimen to the patient; obtaining a second sample from the patient after a time period to ultimately obtain a test level; and detecting in both the first and the second samples the number of SPHK1, EDG4, EDG5, or EDG8 DNA copies per cell, for example, thereby determining the overall or average SPHK1, EDG4, EDG5, or EDG8 gene amplification state in the first and second samples, respectively, wherein a lower number of SPHK1, EDG4, EDG5, or EDG8 DNA copies per cell, for example, in the second sample (test level) than that in the first sample (pre-treatment level) indicates that the treatment regimen is effective.

In yet another aspect, the present invention provides methods for monitoring the efficacy of a therapeutic treatment regimen for treating a cancer (and analogous uses), for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, which comprises, in any practical order, obtaining a first sample from the patient to ultimately obtain a pre-treatment level; administering the treatment regimen to the patient; obtaining a second sample from the patient after a time period to ultimately obtain a test level; contacting the samples with anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 antibodies, and detecting the level of SPHK1, EDG4, EDG5, or EDG8 expression in both the first and the second samples, respectively. A lower level of the SPHK1, EDG4, EDG5, or EDG8 expression in the second sample (test level) than in the first sample (pre-treatment level) indicates that the treatment regimen is effective in the patient.

Yet, in another aspect, the invention provides methods for monitoring the efficacy of a therapeutic treatment regimen for treating a cancer (and analogous uses), for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, comprising, in any practical order, the steps of: obtaining a first sample from the patient to ultimately obtain a pre-treatment level; administering the treatment regimen to the patient; obtaining a second sample from the patient after a time period to ultimately obtain a test level; contacting the samples with anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 antibodies,

determining the level of SPHK1, EDG4, EDG5, or EDG8 expression in both the first and the second samples, by determining the overall expression divided by the number of cells present in each sample; and comparing the expression level of SPHK1, EDG4, EDG5, or EDG8 in the first and the second samples, respectively. A lower level of the SPHK1, EDG4, EDG5, or EDG8 expression in the second sample (test level) than that in the first sample (pre-treatment level) indicates that the treatment regimen is effective in the patient, wherein the expression level can be determined via a binding assay or other appropriate assay.

In still another aspect, the present invention provides methods for monitoring the efficacy of a compound to suppress a cancer (and analogous uses), for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, for example, in a clinical trial or other research studies, which comprises, in any practical order, obtaining a first sample from the patient to ultimately obtain a pre-treatment level; administering the treatment regimen to the patient; obtaining a second sample from the patient after a time period to ultimately obtain a test level; and detecting in both the first and the second samples the number of SPHK1, EDG4, EDG5, or EDG8 DNA copies per cell, for example, thereby determining the SPHK1, EDG4, EDG5, or EDG8 gene amplification state in the first and second samples, respectively, wherein a lower number of SPHK1, EDG4, EDG5, or EDG8 DNA copies per cell, for example, in the second sample (test level) than that in the first sample (pre-treatment level) indicates that the compound is effective.

One aspect of the invention provides methods for diagnosing cancer and/or monitoring the efficacy of a cancer therapy by using an isolated SPHK1, EDG4, EDG5, or EDG8 gene amplicon, wherein the methods further comprise, in any practical order, obtaining a test sample from a region in the tissue that is suspected to be precancerous or cancerous; obtaining a control sample from a region in the tissue or other tissues that is normal; and detecting in both the test sample and the control sample the presence and extent of SPHK1, EDG4, EDG5, or EDG8 gene amplicons, respectively, wherein a level of amplification higher in the test sample than that in the control sample indicates a precancerous or cancerous condition in the tissue. In one aspect, a

control sample can be obtained from a biological subject representative of healthy, cancer-free animals. In another aspect, the control may be obtained from a different individual or be a normalized value based on baseline data obtained from a population.

Another aspect of the invention is to provide an isolated SPHK1, EDG4, EDG5, or EDG8
5 gene amplicon, wherein the amplicon comprises a completely or partially amplified product of SPHK1, EDG4, EDG5, or EDG8 gene, respectively, including a polynucleotide having at least about 90% sequence identity to SPHK1, EDG4, EDG5, or EDG8 gene, for example, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8 or SEQ ID NO:10, or a polynucleotide encoding the polypeptide set forth in SEQ ID NO:2, SEQ ID NO:5, SEQ ID
10 NO:7, or SEQ ID NO:9, or a polynucleotide that is overexpressed in tumor cells having at least about 90% sequence identity to the polynucleotide of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8 or SEQ ID NO:10, or the polynucleotide encoding the polypeptide set forth in SEQ ID NO:2, SEQ ID NO:5, SEQ ID NO:7, or SEQ ID NO:9.

In yet another aspect, the present invention provides methods for modulating SPHK1,
15 EDG4, EDG5, or EDG8 activities by contacting a biological subject from a region that is suspected to be precancerous or cancerous with a modulator of the SPHK1, EDG4, EDG5, or EDG8 protein, respectively, wherein the modulator is, for example, a small molecule.

In still another aspect, the present invention provides methods for modulating SPHK1, EDG4, EDG5, or EDG8 activities by contacting a biological subject from a region that is
20 suspected to be precancerous or cancerous with a modulator of the SPHK1, EDG4, EDG5, or EDG8 protein, wherein said modulator partially or completely inhibits transcription of SPHK1, EDG4, EDG5, or EDG8 gene, respectively.

Another aspect of the invention is to provide methods of making a pharmaceutical composition comprising: identifying a compound which is an inhibitor of SPHK1, EDG4,
25 EDG5, or EDG8 activity, including the oncogenic function or anti-apoptotic activity of SPHK1, EDG4, EDG5, or EDG8, respectively; producing the compound; and optionally mixing the compound with suitable additives or other active agents.

Still another aspect of the invention is to provide a pharmaceutical composition obtainable by the methods described herein, wherein the composition comprises an antibody that blocks the oncogenic function or anti-apoptotic activity of SPHK1, EDG4, EDG5, or EDG8.

Another aspect of the invention is to provide a pharmaceutical composition obtainable by the methods described herein, wherein the composition comprises an antibody that binds to a cell over-expressing SPHK1, EDG4, EDG5, or EDG8 protein, thereby resulting in death or silencing of the cell.

Yet another aspect of the invention is to provide a pharmaceutical composition obtainable by the methods described herein, wherein the composition comprises a SPHK1-, EDG4-, EDG5-, or EDG8-derived polypeptide or a fragment or a mutant thereof, wherein the polypeptide has inhibitory activity that blocks or inhibits the oncogenic function or anti-apoptotic activity of SPHK1, EDG4, EDG5, or EDG8, respectively.

In still a further aspect, the invention provides methods for inducing an immune response in a mammal comprising contacting the mammal with SPHK1, EDG4, EDG5, or EDG8 polypeptide or polynucleotide, or a fragment thereof, wherein the immune response produces antibodies and/or T cell immune response to protect the mammal from cancers, including a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer.

Another aspect of the invention is to provide methods of administering siRNA to a patient in need thereof, wherein the siRNA molecule is delivered in the form of a naked oligonucleotide, sense molecule, antisense molecule, and/or in a vector, wherein the siRNA interacts with SPHK1, EDG4, EDG5, or EDG8 gene or its transcripts, wherein the vector is a plasmid, cosmid, bacteriophage, or a virus, wherein the virus is for example, a retrovirus, an adenovirus, or other suitable viral vector.

Another aspect of the invention is to provide methods of administering miRNA to a patient in need thereof, wherein the miRNA molecule is delivered in the form of a naked oligonucleotide, sense molecule, antisense molecule, and/or in a vector, wherein the miRNA

interacts with SPHK1, EDG4, EDG5, or EDG8 gene or its transcripts, wherein the vector is a plasmid, cosmid, bacteriophage, or a virus, wherein the virus is for example, a retrovirus, an adenovirus, or other suitable viral vector.

Still in another aspect, the invention provides methods of administering a decoy molecule to a patient in need thereof, wherein the molecule is delivered in the form of a naked oligonucleotide, sense molecule, antisense molecule, a decoy DNA molecule, and/or in a vector, wherein the molecule interacts with SPHK1, EDG4, EDG5, or EDG8 gene, wherein the vector is a plasmid, cosmid, bacteriophage, or a virus, wherein the virus is for example, a retrovirus, an adenovirus, or other suitable viral vector.

In still a further aspect of the invention, SPHK1, EDG4, EDG5, or EDG8 decoys, antisense, triple helix forming molecules, and ribozymes can be administered concurrently or consecutively in any proportion; for example, two of the above can be administered concurrently or consecutively in any proportion; or they can be administered singly (that is, decoys, triple helix forming molecules, antisense or ribozymes). Additionally, decoys, triple helix forming molecules, antisense and ribozymes having different sequences but directed against a given target (that is, SPHK1, EDG4, EDG5, or EDG8) can be administered concurrently or consecutively in any proportion, including equimolar proportions. Thus, as is apparent to the skilled person in view of the teachings herein, one could choose to administer one SPHK1, EDG4, EDG5, or EDG8 decoy molecule, triple helix forming molecules, antisense and/or ribozymes, and/or two different SPHK1, EDG4, EDG5, or EDG8 decoys, triple helix forming molecules, antisense and/or ribozymes, and/or three different SPHK1, EDG4, EDG5, or EDG8 decoys, triple helix forming molecules, antisense and/or ribozymes in any proportion, including equimolar proportions, for example. Of course, other permutations and proportions can be employed by the person skilled in the art.

Still in another aspect, the invention provides methods of administering SPHK1-, EDG4-, EDG5-, or EDG8-siRNA and/or -shRNA and/or -miRNA to a patient in need thereof, wherein one or more of the above siRNA and/or shRNA and/or miRNA molecules are delivered in the form of a naked oligonucleotide, sense molecule, antisense molecule or a vector, wherein the

siRNA(s) and/or shRNA(s) and/or miRNA(s) interact(s) with SPHK1, EDG4, EDG5, or EDG8 activity, wherein the vector is a plasmid, cosmid, bacteriophage or a virus, wherein the virus is, for example, a retrovirus, an adenovirus, a poxvirus, a herpes virus or other suitable viral vector. In other words, SPHK1, EDG4, EDG5, or EDG8 siRNAs and/or shRNAs and/or miRNAs can be administered concurrently or consecutively in any proportion; only two of the above can be administered concurrently or consecutively in any proportion; or they can be administered singly (that is, siRNAs or shRNAs or miRNAs targeting SPHK1, EDG4, EDG5, or EDG8). Additionally, siRNAs or shRNAs or miRNAs having different sequences but directed against a given target (that is, SPHK1, EDG4, EDG5, or EDG8) can be administered concurrently or consecutively in any proportion, including equimolar proportions. Thus, as is apparent to the skilled person in view of the teachings herein, one could choose to administer one SPHK1, EDG4, EDG5, or EDG8 siRNA or shRNA or miRNA and/or two different SPHK1, EDG4, EDG5, or EDG8 siRNAs or shRNAs or miRNAs and/or three different SPHK1, EDG4, EDG5, or EDG8 siRNAs or shRNAs or miRNAs in any proportion, including equimolar proportions, for example. Of course, other permutations and proportions can be employed by the person skilled in the art. Additionally, siRNAs or shRNAs or miRNAs can be employed together with one or more of decoys, triple helix forming molecules, antisense, ribozymes, and other functional molecules.

In another aspect, the present invention provides methods of blocking *in vivo* expression of a gene by administering a vector containing SPHK1, EDG4, EDG5, or EDG8 siRNA or shRNA or miRNA, wherein the siRNA and/or shRNA and/or miRNA interacts with SPHK1, EDG4, EDG5, or EDG8 activity, respectively, wherein the siRNA and/or shRNA and/or miRNA causes post-transcriptional silencing of SPHK1, EDG4, EDG5, or EDG8 gene, respectively, or inhibits translation of RNA into protein, in a mammalian cell, for example, a human cell.

Yet, in another aspect, the present invention provides methods of treating cells *ex vivo* by administering a vector as described herein, wherein the vector is a plasmid, cosmid, bacteriophage, or a virus, such as a retrovirus or an adenovirus.

In their *in vivo* or *ex vivo* therapeutic applications, it is appropriate to administer siRNA and/or shRNA and/or miRNA using a viral or retroviral vector which enters the cell by transfection or infection. In particular, as a therapeutic product according to the invention, a vector can be a defective viral vector such as an adenovirus or a defective retroviral vector such as a murine retrovirus.

Another aspect of the invention provides methods of screening a test molecule for SPHK1, EDG4, EDG5, or EDG8 antagonist activity comprising, in any practical order, the steps of: contacting or exposing a cancer cell with the molecule; determining the level of SPHK1, EDG4, EDG5, or EDG8 in the cell, thereby generating data for a test level; and comparing the test level to the level of SPHK1, EDG4, EDG5, or EDG8, respectively, in the cell prior to contacting or exposing the test molecule (initial or pre-exposed level), wherein a decrease in SPHK1, EDG4, EDG5, or EDG8 in the test level indicates SPHK1, EDG4, EDG5, or EDG8 antagonist activity of the test molecule. The level of SPHK1, EDG4, EDG5, or EDG8 is determined by, for example, reverse transcription and polymerase chain reaction (RT-PCR), Northern hybridization, or microarray analysis.

In another aspect, the invention provides methods of screening a test molecule for SPHK1, EDG4, EDG5, or EDG8 antagonist activity comprising the steps of: contacting or exposing the molecule with SPHK1, EDG4, EDG5, or EDG8 and determining the effect of the test molecule on SPHK1, EDG4, EDG5, or EDG8, respectively. The effect can be determined via a binding assay or other appropriate assay, such as RT-PCR, Northern hybridization, or microarray analysis.

In another aspect, the invention provides methods of determining whether a test molecule has SPHK1, EDG4, EDG5, or EDG8 antagonist activity, wherein the method comprises, in any practical order, determining the level of SPHK1, EDG4, EDG5, or EDG8 in a test sample containing cancer cells, thereby generating data for an initial level; contacting the molecule with the test sample to ultimately obtain a test level; and comparing the initial level to the test level, wherein no statistically significant decrease in SPHK1, EDG4, EDG5, or EDG8 in the test level compared to the initial level indicates the test molecule has no SPHK1, EDG4, EDG5, or EDG8

antagonist activity, respectively; and eliminating the test molecule from further evaluation or study.

In another aspect, the invention provides methods for selecting for test molecules having SPHK1, EDG4, EDG5, or EDG8 antagonist activity, wherein the method comprises, in any practical order, determining the level of SPHK1, EDG4, EDG5, or EDG8 in a test sample containing cancer cells, thereby generating data for an initial level; contacting the molecule with the test sample to ultimately obtain a test level; comparing the initial level to the test level, wherein no statistically significant decrease in SPHK1, EDG4, EDG5, or EDG8 in the test level compared to the initial level indicates the test molecule has no SPHK1, EDG4, EDG5, or EDG8 antagonist activity, respectively; and eliminating the test molecule from further evaluation or study.

Yet, in another aspect, the invention provides methods of screening a test molecule for SPHK1, EDG4, EDG5, or EDG8 antagonist activity comprising, in any practical order, the steps of: contacting a test sample containing cancer cells with the test molecule; determining the expression level of SPHK1, EDG4, EDG5, or EDG8 mRNA transcripts per cell, for example, by determining the overall level divided by the number of cells present in the sample, thereby generating data for a test level; and comparing the test level to the expression level of SPHK1, EDG4, EDG5, or EDG8 mRNA transcripts per cell, for example, prior to contacting the test molecule (initial level), wherein a decrease in expression of SPHK1, EDG4, EDG5, or EDG8 in the test level indicates SPHK1, EDG4, EDG5, or EDG8 antagonist activity of the test molecule, respectively. The expression level of SPHK1, EDG4, EDG5, or EDG8 can be determined by, for example, reverse transcription and polymerase chain reaction (RT-PCR), Northern hybridization, or microarray analysis.

Still in another aspect, the invention provides methods of screening a test molecule for SPHK1, EDG4, EDG5, or EDG8 antagonist activity comprising, in any practical order, the steps of: determining the mRNA expression level of SPHK1, EDG4, EDG5, or EDG8 in a test sample containing cancer cells, thereby generating data for an initial or a pre-test level expression of SPHK1, EDG4, EDG5, or EDG8 mRNA; contacting the test sample with the test molecule;

determining the expression level of SPHK1, EDG4, EDG5, or EDG8 mRNA transcripts per cell, for example, by determining the overall level divided by the number of cells present in the sample, thereby generating data for a test level; and comparing the test level to the initial or pre-test level expression of SPHK1, EDG4, EDG5, or EDG8 mRNA transcripts per cell, for example, wherein a decrease in expression of SPHK1, EDG4, EDG5, or EDG8 mRNA in the test level indicates SPHK1, EDG4, EDG5, or EDG8 antagonist activity of the test molecule, respectively. The expression level of SPHK1, EDG4, EDG5, or EDG8 can be determined by, for example, reverse transcription and polymerase chain reaction (RT-PCR), Northern hybridization, or microarray analysis.

10 In another aspect, the invention provides methods for determining the level of SPHK1, EDG4, EDG5, or EDG8 in a test sample for diagnosis of a cancer, for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in a patient, comprising, in any practical order, obtaining a control sample; obtaining a test sample from the patient; contacting both the control and the test samples with anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 antibodies, determining the level of SPHK1, EDG4, EDG5, or EDG8 in both the control and the test samples, by determining the overall level of SPHK1, EDG4, EDG5, or EDG8 divided by the number of cells present in each sample; and comparing the level of SPHK1, EDG4, EDG5, or EDG8, respectively, in the control and the test samples. A higher level of the SPHK1, EDG4, EDG5, or EDG8 in the test sample obtained from the patient than that in the control sample indicates a cancer or a precancerous condition. The SPHK1, EDG4, EDG5, or EDG8 level can be determined via binding assays or other appropriate assays, such as RT-PCR, Northern hybridization, or microarray analysis. Alternatively, a given level of SPHK1, EDG4, EDG5, or EDG8, representative of the cancer-free population, that has been previously established based on measurements from normal, cancer-free animals, can be used as a control. A control data point from a reference database, based on data obtained from control samples representative of a cancer-free population, also can be used as a control.

In another aspect, the invention provides methods for determining the efficacy of a therapeutic treatment regimen in a patient, comprising, in any practical order, measuring at least one of SPHK1, EDG4, EDG5, or EDG8 mRNA or SPHK1, EDG4, EDG5, or EDG8 protein expression levels in a first sample obtained from the patient, thereby generating data for a pre-treatment level; administering the treatment regimen to the patient; measuring at least one of SPHK1, EDG4, EDG5, or EDG8 mRNA or SPHK1, EDG4, EDG5, or EDG8 protein expression levels in a second sample from the patient at a time following administration of the treatment regimen (test level); and comparing at least one of SPHK1, EDG4, EDG5, or EDG8 mRNA or SPHK1, EDG4, EDG5, or EDG8 protein expression levels in the first and the second samples, respectively. Data showing no statistically significant decrease in the levels in the second sample relative to the first sample indicates that the treatment regimen is not effective in the patient.

In another aspect, the invention provides methods for selecting test molecules having a therapeutic effect in a patient, comprising, in any practical order, measuring at least one of SPHK1, EDG4, EDG5, or EDG8 mRNA or SPHK1, EDG4, EDG5, or EDG8 protein expression levels in a first sample obtained from the patient, thereby generating data for a pre-treatment level; administering the test molecule to the patient; measuring at least one of SPHK1, EDG4, EDG5, or EDG8 mRNA or SPHK1, EDG4, EDG5, or EDG8 protein expression levels in a second sample from the patient at a time following administration of the test molecule, thereby generating a test level; comparing at least one of SPHK1, EDG4, EDG5, or EDG8 mRNA or SPHK1, EDG4, EDG5, or EDG8 protein expression levels in the first and the second samples, respectively. Data showing no statistically significant decrease in the levels in the second sample (test level) relative to the first sample (pre-treatment level) indicates that the test molecule is not effective in the patient; and eliminating the test molecule from further evaluation or study.

Samples can be obtained from the same region or a different region of a subject. Typically, samples are taken in regions that are similar in terms of organ or tissue type and location in order to minimize variables.

Yet, in another aspect, the present invention provides methods for treating cancer or precancerous growth in a mammalian tissue, comprising contacting the tissue with an antibody to S1P protein, wherein the antibody binds to S1P protein, and wherein the tissue comprises a colon tissue, an ovarian tissue, a breast tissue, a lung tissue, a brain tissue, a kidney tissue, a head and neck tissue, a stomach tissue, an esophagus tissue, and a bladder tissue.

Still in another aspect, the invention provides methods of treating cancer in a patient comprising administering the patient an effective amount of a S1P-antibody, wherein the antibody is a blocking antibody to S1P, and wherein the cancer is a colon cancer, an ovarian cancer, a breast cancer, a lung cancer, a brain cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer.

The compounds, targets, assays, tests, inquiries and methodologies described herein can be employed in a variety of contexts, including diagnostic and therapeutic discovery, diagnostic and therapeutic development, safety and efficacy monitoring, treatment assessment, comparative studies, marketing and the like. The information provided by the invention can be communicated to regulators, physicians and other healthcare providers, manufacturers, owners, investors, patients, and/or the general public. This information and the like can be used in exploratory research, pre-clinical and clinical settings, labeling, production, advertising, and sales, for example.

Unless otherwise defined, all technical and scientific terms used herein in their various grammatical forms have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar to those described herein can be used in the practice or testing of the present invention, the preferred methods and materials are described below. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and are not limiting.

Further features, objects, and advantages of the present invention are apparent in the claims and the detailed description that follows. It should be understood, however, that the detailed description and the specific examples, while indicating preferred aspects of the

invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

5 **BRIEF DESCRIPTION OF THE DRAWING**

Figure 1 shows EDG4 amplification in breast, colon, lung, ovarian, head and neck, liver, kidney, stomach, and esophagus tumors. Solid circles in each column indicate number of tumor samples with >3X amplification of EDG4.

10 **Figure 2** shows EDG4 overexpression in breast, colon, lung, ovarian, head and neck, liver, kidney, stomach, and prostate tumors. Solid circles in each column indicate number of tumor samples with >5X overexpression of EDG4.

Figure 3 depicts the epicenter mapping of human chromosome region 19p12 amplicon, which includes EDG4 locus. The number of DNA copies for each sample is plotted on the Y-axis, and the X-axis corresponds to nucleotide position based on Human Genome Project
15 working draft sequence (<http://genome.ucsc.edu/goldenPath/aug2001Tracks.html>).

Figure 4 depicts the epicenter mapping of human chromosome region 19p13 amplicon, which includes EDG5 and EDG8 loci. EDG5 is located at about 100 kilo bases from EDG8 in chromosome 19p13.3. The number of DNA copies for each sample is plotted on the Y-axis, and the X-axis corresponds to nucleotide position based on Human Genome Project working draft
20 sequence (<http://genome.ucsc.edu/goldenPath/aug2001Tracks.html>).

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides methods and compositions for the diagnosis, prevention, and treatment of tumors and cancers, for example, a colon cancer, an ovarian cancer, a brain
25 cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, in mammals, for example, humans.

The invention is based on the findings of novel traits of the SPHK1, EDG4, EDG5, and EDG8 genes. The SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 genes and their expressed protein products can thus be used diagnostically or as targets for therapy; and, they also can be used to identify compounds useful in the diagnosis, prevention, and therapy of tumors and cancers (for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer).

Sphingosine kinase 1 (SPHK1) and Sphingosine 1-phosphate (S1P):

SPHK1 is a highly conserved lipid kinase that catalyzes the phosphorylation of sphingosine to form sphingosine-1-phosphate (S1P). SPHK1 is located on human chromosome 17q25.2. S1P and SPHK1 have been implicated in a signalling pathway that regulates diverse cellular functions, including cell growth, proliferation and survival. S1P is a lipid messenger with both intracellular and extracellular functions. Intracellularly, S1P regulates proliferation and survival, and extracellularly, it is a ligand for EDG family G-protein coupled receptors. It has been reported that SPHK1 gene can act as an oncogene (see, for example, WO 01/85953; Xia *et al.*, *Curr Biol.* 10(23):1527-30, 2000; Liu *et al.*, *Progress in Nucleic Acid Research and Molecular Biology* 71:493-511, 2002). It also has been reported that cells overexpressing SPHK1 can increase enzymatic activity and acquire a transformed phenotype, as determined by focus formation, colony growth in soft agar, and the ability to form tumours in nude mice (see Xia *et al.*, *Curr Biol.* 10(23):1527-30, 2000). Several international and US publications describe aspects of SPHK1 gene and polypeptide (see for example, WO 01/31029, WO 00/55332, WO 00/70028, WO 01/53312, WO 00/52173, WO 01/60990, WO 99/12533, WO 99/61581, WO 98/54963, EP1074617, and US Patent Application Publication No. 2002042358). However, its role in tumorigenesis, amplification and overexpression of the SPHK1 gene in cancers has not been discussed.

Sphingosine 1-phosphate (S1P) and *Homo sapiens* endothelial differentiation gene (EDG), sphingolipid G-protein coupled receptors 4, 5, and 8 (EDG4, EDG5, and EDG8):

Sphingosine 1-phosphate (S1P), a lysophospholipid, is known to be involved in cell signaling through a set of G-protein coupled receptors designated as EDG (endothelial differentiation gene)-receptors. The EDG-family of G-protein coupled receptors currently comprises eight human members (EDG1 to EDG8) that fall into two major groups depending on their preference for the activating lipid-ligand: EDG1, EDG3, EDG5, EDG6 and EDG8 preferentially interact with S1P (Molderings *et al.*, *Neurochem Int.* 40(2):157-67, 2002; Liliom *et al.*, *Biochem J.* 2001 355(Pt 1):189-97, 2001; Pyne *et al.*, *Biochem J* 349(Pt 2):385-402, 2000; Yatom *et al.*, *J Biochem* (Tokyo) 12:969, 1997; Lee *et al.*, *Science* 279:1552, 1998; Lee *et al.*, *J Biol Chem* 273:22105, 1998; Ancellin and Hla, *J Biol Chem* 274:18997, 1999; Yamazaki *et al.*, *Biochem Biophys Res Commun* 268:583, 2000; Van Brocklyn *et al.*, *Blood* 95:2624, 2000), EDG2, EDG4 and EDG7 preferentially interact with lysophosphatidic acid (LPA) (An *et al.*, *J Biol Chem* 273:7906, 1998; Im *et al.*, *Mol Pharmacol* 57:753, 2000).

Both LPA and S1P are recognized to signal cells through a set of G-protein coupled receptors (GPCRs) known as EDG. Recent investigation has revealed that LPA acts via a single family of GPCRs, EDGs, which include EDG2 (LPA1), EDG4 (LPA2) and EDG7 (LPA3). Each receptor isoform displays a unique tissue expression pattern and can couple to at least 3 distinct G proteins (Gq, Gi and G_{12/13}) leading to activation of multiple intracellular signaling pathways such as PI signaling, activation of Ras and the Rho GTPases cascades (An *et al.*, *J Biol Chem* 273:7906, 1998; Contos *et al.*, *Mol Cell Biol* 22:6921-6929, 2002; Mills *et al.*, *Nature Rev Cancer* 3:582-591, 2003). LPA is known to be involved in the initiation, progression and metastases of ovarian cancer and EDG4 is overexpressed in differentiated thyroid cancer. There is a correlation between EDG4 and VEGF expression in ovarian cancer. It has been suggested that EDG4 may play a role in LPA stimulation of ovarian tumor growth. A recent report also suggests that cyclin D1 may act on downstream of LPA receptors. Homozygous EDG4 knockout mice; however, displayed no abnormal phenotype (Fujita *et al.*, *Cancer Lett* 192:161-169, 2003; Hu *et al.*, *J Natl Cancer Inst* 93:762-768, 2001; Hu *et al.*, *J Natl Cancer Inst* 95:733-740, 2003;

Mills *et al.*, *Cancer Treat Res* 107:259-283, 2002; Schulte *et al.*, *Int J Cancer* 92:249-256, 2001; Fang *et al.*, *Ann N Y Acad Sci* 905:188-208, 2000).

S1P is implicated in a wide spectrum of biological activities, including stimulation of cell growth, regulation of actin cytoskeleton, modulation of cell shape, cell migration, cell proliferation, modulation of cell motility (Takuwa *et al.*, *J Biochem* (Tokyo) 131:767-771, 2002; Hla *et al.*, *Biochem Pharm* 58:201, 1999), induction/suppression of apoptosis (Hisano *et al.*, *Blood* 93:4293, 1999; Xia *et al.*, *J Biol Chem* 274:34499, 1999), angiogenesis (Lee *et al.*, *Cell* 99:301, 1999), tumor invasiveness (Sadahira *et al.*, *PNAS USA* 89:9686, 1992), platelet activation (Gueguen *et al.*, *Biochemistry* 38: 8440, 1999) and neurite retraction (Postma *et al.*, *EMBO J* 15:2388, 1996).

As noted above, EDG5 and EDG8, along with EDG1, EDG3, and EDG6, are G-protein coupled receptors for sphingosine-1-phosphate (S1P). Each receptor isoform displays a unique tissue expression pattern and coupling to a distinct set of heterotrimeric G-proteins, leading to the activation of an isoform-specific panel of multiple intracellular signaling pathways. Recent studies on knockout mice have unveiled non-redundant EDG receptor functions that are essential for normal development and vascular maturation. In addition, the EDG lysophospholipid signaling system may play a role in modulating cell motility under pathological conditions such as inflammation, tumor cell dissemination and vascular remodeling (Takuwa *et al.*, *J Biochem* (Tokyo) 131(6):767-771, 2002).

Several U. S. and international patents and applications describe aspects of EDG4, EDG5, EDG8 and related molecules. U.S. Patent Nos. 6,037,146 (EP 0 855 443); 6,020,158 (based on WO 98/53062); 6,482,609 (based on WO 99/35259); 5,998,164; 6,090,575; 6,485,922; U.S. Patent Publication No. 2002090691; WO 96/30406; WO 01/12838; WO 99/19513; WO 00/56135; WO 02/61087; and WO 02/12342 describe general aspects of EDG4 related polypeptide, encoding nucleotides, methods of making molecules and use of the molecules in treating various diseases. WO 02/27028 discloses methods of determining copy number or expression level of EDG related genes that are associated with lipid metabolism and synthesis.

Goetzl *et al.* (WO 00/56135), Bergsma *et al.* (WO 99/54351) and Munroe *et al.* (WO 99/35259) describe general aspects of EDG5, related polypeptide, encoding nucleotides and use of molecules that can inhibit EDG expression. WO 01/04139 and EP1090925 describe methods of identifying agonists and antagonists for Axor29, an EDG-family receptor. WO 00/11166
5 discloses nucleotides, polypeptides and expression of 14274 (EDG family) receptor. WO 00/22131, WO 00/31258, and WO 01/66742 describe cDNA encoding endogenous and non-endogenous receptors of human G-protein coupled receptors and a method of treatment associated with decreased expression. WO 01/81573 discloses nucleotides and polypeptides of EDG8, and a process of disease diagnosis by analyzing its presence. However, amplification and
10 overexpression of SPHK1, EDG4, EDG5, or EDG8 gene and their practical uses in cancer diagnosis and treatment have not been discussed.

The present invention also provides isolated amplified SPHK1, EDG4, EDG5, and EDG8 genes. This invention also provides that the SPHK1, EDG4, EDG5, and EDG8 genes are frequently amplified and/or overexpressed in tumor cells, for example, human colon tumor,
15 ovarian tumor, brain tumor, breast tumor, lung tumor, liver tumor, kidney tumor, head and neck tumor, stomach tumor, esophagus tumor, and bladder tumor, and relates to methods and compositions associated with the diagnosis, prevention, monitoring, and treatment of cancers.

1. **Definitions:**

20 A "**cancer**" in an animal refers to the presence of cells possessing characteristics typical of cancer-causing cells, for example, uncontrolled proliferation, loss of specialized functions, immortality, significant metastatic potential, significant increase in anti-apoptotic activity, rapid growth and proliferation rate, and certain characteristic morphology and cellular markers. In some circumstances, cancer cells will be in the form of a tumor; such cells may exist locally
25 within an animal, or circulate in the blood stream as independent cells, for example, leukemic cells.

The phrase "**detecting a cancer**" or "**diagnosing a cancer**" refers to determining the presence or absence of cancer or a precancerous condition in an animal. "Detecting a cancer" also can refer to obtaining indirect evidence regarding the likelihood of the presence of precancerous or cancerous cells in the animal or assessing the predisposition of a patient to the development of a cancer. Detecting a cancer can be accomplished using the methods of this invention alone, in combination with other methods, or in light of other information regarding the state of health of the animal.

A "**tumor**," as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all precancerous and cancerous cells and tissues.

The term "**precancerous**" refers to cells or tissues having characteristics relating to changes that may lead to malignancy or cancer. Examples include adenomatous growths in colonic, ovarian, brain, breast, lung, liver, kidney, or bladder, tissues, or conditions, for example, dysplastic nevus syndrome, a precursor to malignant melanoma of the skin. Examples also include, abnormal neoplastic, in addition to dysplastic nevus syndromes, polyposis syndromes, prostatic dysplasia, and other such neoplasms, whether the precancerous lesions are clinically identifiable or not.

A "**differentially expressed gene transcript**", as used herein, refers to a gene, including an oncogene, transcript that is found in different numbers of copies in different cell or tissue types of an organism having a tumor or cancer, for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, compared to the numbers of copies or state of the gene transcript found in the cells of the same tissue in a healthy organism, or in the cells of the same tissue in the same organism. Multiple copies of gene transcripts may be found in an organism having the tumor or cancer, while fewer copies of the same gene transcript are found in a healthy organism or healthy cells of the same tissue in the same organism, or *vice-versa*.

A "differentially expressed gene," can be a target, fingerprint, or pathway gene. For example, a "**fingerprint gene**", as used herein, refers to a differentially expressed gene whose

expression pattern can be used as a prognostic or diagnostic marker for the evaluation of tumors and cancers, or which can be used to identify compounds useful for the treatment of tumors and cancers, for example, colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, or bladder cancer. For example, the effect of a compound on the fingerprint gene expression pattern normally displayed in connection with tumors and cancers can be used to evaluate the efficacy of the compound as a tumor and cancer treatment, or can be used to monitor patients undergoing clinical evaluation for the treatment of tumors and cancer.

A "**fingerprint pattern**", as used herein, refers to a pattern generated when the expression pattern of a series (which can range from two up to all the fingerprint genes that exist for a given state) of fingerprint genes is determined. A fingerprint pattern also may be referred to as an "**expression profile**". A fingerprint pattern or expression profile can be used in the same diagnostic, prognostic, and compound identification methods as the expression of a single fingerprint gene.

A "**target gene**", as used herein, refers to a differentially expressed gene in which modulation of the level of gene expression or of gene product activity prevents and/or ameliorates tumor and cancer, for example, colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, or bladder cancer, symptoms. Thus, compounds that modulate the expression of a target gene, the target gene, or the activity of a target gene product can be used in the diagnosis, treatment or prevention of tumors and cancers. A particular target gene of the present invention is the SPHK1, EDG4, EDG5, or EDG8 gene.

In general, a "**gene**" is a region on the genome that is capable of being transcribed to an RNA that either has a regulatory function, a catalytic function, and/or encodes a protein. An eukaryotic gene typically has introns and exons, which may organize to produce different RNA splice variants that encode alternative versions of a mature protein. The skilled artisan will appreciate that the present invention encompasses all SPHK1-, EDG4-, EDG5-, and EDG8-encoding transcripts that may be found, including splice variants, allelic variants and transcripts

that occur because of alternative promoter sites or alternative poly-adenylation sites. A "**full-length**" gene or RNA therefore encompasses any naturally occurring splice variants, allelic variants, other alternative transcripts, splice variants generated by recombinant technologies which bear the same function as the naturally occurring variants, and the resulting RNA molecules. A "**fragment**" of a gene, including an oncogene, can be any portion from the gene, which may or may not represent a functional domain, for example, a catalytic domain, a DNA binding domain, *etc.* A fragment may preferably include nucleotide sequences that encode for at least 25 contiguous amino acids, and preferably at least about 30, 40, 50, 60, 65, 70, 75 or more contiguous amino acids or any integer thereabout or therebetween.

"**Pathway genes**", as used herein, are genes that encode proteins or polypeptides that interact with other gene products involved in tumors and cancers. Pathway genes also can exhibit target gene and/or fingerprint gene characteristics.

A "**detectable**" RNA expression level, as used herein, means a level that is detectable by standard techniques currently known in the art or those that become standard at some future time, and include for example, differential display, RT (reverse transcriptase)-coupled polymerase chain reaction (PCR), Northern Blot, and/or RNase protection analyses. The degree of differences in expression levels need only be large enough to be visualized or measured via standard characterization techniques.

As used herein, the term "**transformed cell**" means a cell into which (or into predecessor or an ancestor of which) a nucleic acid molecule encoding a polypeptide of the invention has been introduced, by means of, for example, recombinant DNA techniques or viruses.

The nucleic acid molecules of the invention, for example, the SPHK1, EDG4, EDG5, and EDG8 genes or their subsequences, can be inserted into a vector, as described below, which will facilitate expression of the insert. The nucleic acid molecules and the polypeptides they encode can be used directly as diagnostic or therapeutic agents, or can be used (directly in the case of the polypeptide or indirectly in the case of a nucleic acid molecule) to generate antibodies that, in turn, are clinically useful as a therapeutic or diagnostic agent. Accordingly, vectors containing the nucleic acids of the invention, cells transfected with these vectors, the polypeptides

expressed, and antibodies generated against either the entire polypeptide or an antigenic fragment thereof, are among the aspects of the invention.

A "**structural gene**" is a DNA sequence that is transcribed into messenger RNA (mRNA) which is then translated into a sequence of amino acids characteristic of a specific polypeptide.

An "**isolated DNA molecule**" is a fragment of DNA that has been separated from the chromosomal or genomic DNA of an organism. Isolation also is defined to connote a degree of separation from original source or surroundings. For example, a cloned DNA molecule encoding an avidin gene is an isolated DNA molecule. Another example of an isolated DNA molecule is a chemically-synthesized DNA molecule, or enzymatically-produced cDNA, that is not integrated in the genomic DNA of an organism. Isolated DNA molecules can be subjected to procedures known in the art to remove contaminants such that the DNA molecule is considered purified, that is, towards a more homogeneous state.

"**Complementary DNA**" (cDNA), often referred to as "copy DNA", is a single-stranded DNA molecule that is formed from an mRNA template by the enzyme reverse transcriptase. Typically, a primer complementary to portions of the mRNA is employed for the initiation of reverse transcription. Those skilled in the art also use the term "cDNA" to refer to a double-stranded DNA molecule that comprises such a single-stranded DNA molecule and its complement DNA strand.

The term "**expression**" refers to the biosynthesis of a gene product. For example, in the case of a structural gene, expression involves transcription of the structural gene into mRNA and the translation of mRNA into one or more polypeptides.

The term "**amplification**" refers to amplification, duplication, multiplication, or multiple expression of nucleic acids or a gene, *in vivo*, *ex-vivo*, or *in vitro*, yielding about 3.0 fold or more copies. For example, amplification of the SPHK1, EDG4, EDG5, or EDG8 gene resulting in a copy number greater than or equal to 3.0 is deemed to have been amplified. However, an increase in SPHK1, EDG4, EDG5, or EDG8 gene copy number less than 3.0 fold can still be

considered as an amplification of the gene. The 3.0 fold figure is due to current detection limit, rather than a biological state.

The term "**amplicon**" refers to an amplification product containing one or more genes, which can be isolated from a precancerous or a cancerous cell or a tissue. SPHK1, EDG4, EDG5, or EDG8 amplicon is a result of amplification, duplication, multiplication, or multiple expression of nucleic acids or a gene, *in vivo*, *ex-vivo*, or *in vitro*. "Amplicon", as defined herein, also includes a completely or partially amplified SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 genes. For example, an amplicon comprising a polynucleotide having at least about 90% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8 or SEQ ID NO:10, or a fragment thereof.

A "**cloning vector**" is a nucleic acid molecule, for example, a plasmid, cosmid, or bacteriophage that has the capability of replicating autonomously in a host cell. Cloning vectors typically contain (i) one or a small number of restriction endonuclease recognition sites at which foreign DNA sequences can be inserted in a determinable fashion without loss of an essential biological function of the vector, and (ii) a marker gene that is suitable for use in the identification and selection of cells transformed or transfected with the cloning vector. Marker genes include genes that provide tetracycline resistance or ampicillin resistance, for example.

An "**expression vector**" is a nucleic acid construct, generated recombinantly or synthetically, bearing a series of specified nucleic acid elements that enable transcription of a particular gene in a host cell. Typically, gene expression is placed under the control of certain regulatory elements, including constitutive or inducible promoters, tissue-preferred regulatory elements, and enhancers.

A "**recombinant host**" may be any prokaryotic or eukaryotic cell that contains either a cloning vector or expression vector. This term also includes those prokaryotic or eukaryotic cells that have been genetically engineered to contain the cloned gene(s) in the chromosome or genome of the host cell.

"**Antisense RNA**": In eukaryotes, RNA polymerase catalyzes the transcription of a structural gene to produce mRNA. A DNA molecule can be designed to contain an RNA polymerase template in which the RNA transcript has a sequence that is complementary to that of a preferred mRNA. The RNA transcript is termed an "**antisense RNA**". Antisense RNA molecules can inhibit mRNA expression (for example, Rylova *et al.*, *Cancer Res*, 62(3):801-8, 2002; Shim *et al.*, *Int. J. Cancer*, 94(1):6-15, 2001).

"**Antisense DNA**" or "**DNA decoy**" or "**decoy molecule**": With respect to a first nucleic acid molecule, a second DNA molecule or a second chimeric nucleic acid molecule that is created with a sequence which is a complementary sequence or homologous to the complementary sequence of the first molecule or portions thereof, is referred to as the "**antisense DNA**" or "**DNA decoy**" or "**decoy molecule**" of the first molecule. The term "**decoy molecule**" also includes a nucleic acid molecule, which may be single or double stranded, that comprises DNA or PNA (peptide nucleic acid) (Mischianti *et al.*, *Int. J. Mol. Med.*, 9(6):633-9, 2002), and that contains a sequence of a protein binding site, preferably a binding site for a regulatory protein and more preferably a binding site for a transcription factor. Applications of antisense nucleic acid molecules, including antisense DNA and decoy DNA molecules are known in the art, for example, Morishita *et al.*, *Ann. N Y Acad. Sci.*, 947:294-301, 2001; Andratschke *et al.*, *Anticancer Res*, 21:(5)3541-3550, 2001. Antisense DNA or PNA molecules can inhibit, block, or regulate function and/or expression of a SPHK1, an EDG4, an EDG5, or an EDG8 gene. Antisense and decoys can have different sequences, but can be directed against a SPHK1, an EDG4, an EDG5, or an EDG8 and can be administered concurrently or consecutively in any proportion, including equimolar proportions.

The term "**operably linked**" is used to describe the connection between regulatory elements and a gene or its coding region. That is, gene expression is typically placed under the control of certain regulatory elements, including constitutive or inducible promoters, tissue-specific regulatory elements, and enhancers. Such a gene or coding region is said to be "operably linked to" or "operatively linked to" or "operably associated with" the regulatory

elements, meaning that the gene or coding region is controlled or influenced by the regulatory element.

"**Sequence homology**" is used to describe the sequence relationships between two or more nucleic acids, polynucleotides, proteins, or polypeptides, and is understood in the context of and in conjunction with the terms including: (a) reference sequence, (b) comparison window, (c) sequence identity, (d) percentage of sequence identity, and (e) substantial identity or "homologous."

(a) A "**reference sequence**" is a defined sequence used as a basis for sequence comparison. A reference sequence may be a subset of or the entirety of a specified sequence; for example, a segment of a full-length cDNA or gene sequence, or the complete cDNA or gene sequence. For polypeptides, the length of the reference polypeptide sequence will generally be at least about 16 amino acids, preferably at least about 20 amino acids, more preferably at least about 25 amino acids, and even more preferably about 35 amino acids, about 50 amino acids, or about 100 amino acids. For nucleic acids, the length of the reference nucleic acid sequence will generally be at least about 50 nucleotides, preferably at least about 60 nucleotides, more preferably at least about 75 nucleotides, and even more preferably about 100 nucleotides or about 300 nucleotides or any integer thereabout or therebetween.

(b) A "**comparison window**" includes reference to a contiguous and specified segment of a polynucleotide sequence, wherein the polynucleotide sequence may be compared to a reference sequence and wherein the portion of the polynucleotide sequence in the comparison window may comprise additions, substitutions, or deletions (*i.e.*, gaps) compared to the reference sequence (which does not comprise additions, substitutions, or deletions) for optimal alignment of the two sequences. Generally, the comparison window is at least 20 contiguous nucleotides in length, and optionally can be 30, 40, 50, 100, or longer. Those of skill in the art understand that to avoid a misleadingly high similarity to a reference sequence due to inclusion of gaps in the polynucleotide sequence a gap penalty is typically introduced and is subtracted from the number of matches.

Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman, *Adv. Appl. Math.*, 2: 482, 1981; by the homology alignment algorithm of Needleman and Wunsch, *J. Mol. Biol.*, 48: 443, 1970; by the search for similarity method of Pearson and Lipman, *Proc. Natl. Acad. Sci. USA*, 8: 2444, 1988; by computerized implementations of these algorithms, including, but not limited to: CLUSTAL in the PC/Gene program by Intelligenetics, Mountain View, California, GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 7 Science Dr., Madison, Wisconsin, USA; the CLUSTAL program is well described by Higgins and Sharp, *Gene*, 73: 237-244, 1988; Corpet, *et al.*, *Nucleic Acids Research*, 16:881-90, 1988; Huang, *et al.*, *Computer Applications in the Biosciences*, 8:1-6, 1992; and Pearson, *et al.*, *Methods in Molecular Biology*, 24:7-331, 1994. The BLAST family of programs which can be used for database similarity searches includes: BLASTN for nucleotide query sequences against nucleotide database sequences; BLASTX for nucleotide query sequences against protein database sequences; BLASTP for protein query sequences against protein database sequences; TBLASTN for protein query sequences against nucleotide database sequences; and TBLASTX for nucleotide query sequences against nucleotide database sequences. See, *Current Protocols in Molecular Biology*, Chapter 19, Ausubel, *et al.*, Eds., Greene Publishing and Wiley-Interscience, New York, 1995. New versions of the above programs or new programs altogether will undoubtedly become available in the future, and can be used with the present invention.

Unless otherwise stated, sequence identity/similarity values provided herein refer to the value obtained using the BLAST 2.0 suite of programs, or their successors, using default parameters. Altschul *et al.*, *Nucleic Acids Res*, 2:3389-3402, 1997. It is to be understood that default settings of these parameters can be readily changed as needed in the future.

As those ordinary skilled in the art will understand, BLAST searches assume that proteins can be modeled as random sequences. However, many real proteins comprise regions of nonrandom sequences which may be homopolymeric tracts, short-period repeats, or regions enriched in one or more amino acids. Such low-complexity regions may be aligned between

unrelated proteins even though other regions of the protein are entirely dissimilar. A number of low-complexity filter programs can be employed to reduce such low-complexity alignments. For example, the SEG (Wooten and Federhen, *Comput. Chem.*, 17:149-163, 1993) and XNU (Claverie and States, *Comput. Chem.*, 17:191-1, 1993) low-complexity filters can be employed alone or in combination.

(c) "**Sequence identity**" or "**identity**" in the context of two nucleic acid or polypeptide sequences includes reference to the residues in the two sequences which are the same when aligned for maximum correspondence over a specified comparison window, and can take into consideration additions, deletions and substitutions. When percentage of sequence identity is used in reference to proteins it is recognized that residue positions which are not identical often differ by conservative amino acid substitutions, where amino acid residues are substituted for other amino acid residues with similar chemical properties (for example, charge or hydrophobicity) and therefore do not deleteriously change the functional properties of the molecule. Where sequences differ in conservative substitutions, the percent sequence identity may be adjusted upwards to correct for the conservative nature of the substitution. Sequences which differ by such conservative substitutions are said to have sequence similarity. Approaches for making this adjustment are well-known to those of skill in the art. Typically this involves scoring a conservative substitution as a partial rather than a full mismatch, thereby increasing the percentage sequence identity. Thus, for example, where an identical amino acid is given a score of 1 and a non-conservative substitution is given a score of zero, a conservative substitution is given a score between zero and 1. The scoring of conservative substitutions is calculated, for example, according to the algorithm of Meyers and Miller, *Computer Applic. Biol. Sci.*, 4: 11-17, 1988, for example, as implemented in the program PC/GENE (Intelligenetics, Mountain View, California, USA).

(d) "**Percentage of sequence identity**" means the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions, substitutions, or deletions (*i.e.*, gaps) as compared to the reference sequence (which does not comprise additions,

substitutions, or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity.

(e) (i) The term "**substantial identity**" or "**homologous**" in their various grammatical forms in the context of polynucleotides means that a polynucleotide comprises a sequence that has a desired identity, for example, at least 60% identity, preferably at least 70% sequence identity, more preferably at least 80%, still more preferably at least 90% and even more preferably at least 95%, compared to a reference sequence using one of the alignment programs described using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means sequence identity of at least 60%, more preferably at least 70%, 80%, 90%, and even more preferably at least 95%.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other under stringent conditions. However, nucleic acids which do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This may occur, for example, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. One indication that two nucleic acid sequences are substantially identical is that the polypeptide which the first nucleic acid encodes is immunologically cross reactive with the polypeptide encoded by the second nucleic acid, although such cross-reactivity is not required for two polypeptides to be deemed substantially identical.

(e) (ii) The term "**substantial identity**" or "**homologous**" in their various grammatical forms in the context of peptides indicates that a peptide comprises a sequence that has a desired identity, for example, at least 60% identity, preferably at least 70% sequence identity to a

reference sequence, more preferably 80%, still more preferably 85%, even more preferably at least 90% or 95% sequence identity to the reference sequence over a specified comparison window. Preferably, optimal alignment is conducted using the homology alignment algorithm of Needleman and Wunsch, *J. Mol. Biol.*, 48:443, 1970. An indication that two peptide sequences are substantially identical is that one peptide is immunologically reactive with antibodies raised against the second peptide, although such cross-reactivity is not required for two polypeptides to be deemed substantially identical. Thus, a peptide is substantially identical to a second peptide, for example, where the two peptides differ only by a conservative substitution. Peptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative substitutions typically include, but are not limited to, substitutions within the following groups: glycine and alanine; valine, isoleucine, and leucine; aspartic acid and glutamic acid; asparagine and glutamine; serine and threonine; lysine and arginine; and phenylalanine and tyrosine, and others as known to the skilled person.

"Biological subject" as used herein refers to a target biological object obtained, reached, or collected *in vivo*, *ex-vivo*, or *in situ*, that contains or is suspected of containing nucleic acids or polypeptides of SPHK1, EDG4, EDG5, or EDG8. A biological subject is typically of eukaryotic nature, for example, insects, protozoa, birds, fish, reptiles, and preferably a mammal, for example, rat, mouse, cow, dog, guinea pig, or rabbit, and more preferably a primate, for example, chimpanzees, or humans such as a patient in need of diagnostic review, treatment and/or monitoring of therapy.

"Biological sample" as used herein refers to a sample obtained from a biological subject, including sample of biological tissue or fluid origin, obtained, reached, or collected *in vivo*, *ex-vivo*, or *in situ*, that contains or is suspected of containing nucleic acids or polypeptides of SPHK1, EDG4, EDG5, or EDG8. A biological sample also includes samples from a region of a biological subject containing precancerous or cancer cells or tissues. Such samples can be, but are not limited to, organs, tissues, fractions and cells isolated from mammals including, humans such as a patient, mice, and rats. Biological samples also may include sections of the biological

sample including tissues, for example, frozen sections taken for histologic purposes. A biological sample is typically of an eukaryotic origin, for example, insects, protozoa, birds, fish, reptiles, and preferably a mammal, for example, rat, mouse, cow, dog, guinea pig, or rabbit, and more preferably a primate, for example, chimpanzees or humans. A biological sample, as described herein, can be: a "control" or a "control sample" or a "test sample".

A "**control**" refers to a representative of healthy, cancer-free biological subject or information obtained from a different individual or a normalized value, which can be based on baseline data obtained from a population or other acceptable sources. A control also can refer to a given level of SPHK1, EDG4, EDG5, or EDG8, representative of the cancer-free population, that has been previously established based on measurements from normal, cancer-free animals. A control also can be a reference data point in a database based on data obtained from control samples representative of a cancer-free population. Further, a control can be established by a specific age, sex, ethnicity or other demographic parameters. In some situations, the control is implicit in the particular measurement. A typical control level for a gene is two copies per cell. An example of an implicit control is where a detection method can only detect SPHK1, EDG4, EDG5, or EDG8, or the corresponding gene copy number, when a level higher than that typical of a normal, cancer-free animal is present. Another example is in the context of an immunohistochemical assay where the control level for the assay is known. Other instances of such controls are within the knowledge of the skilled person.

A "**control sample**" refers to a sample of biological material representative of healthy, cancer-free animals or a normal biological subject obtained from a cancer-free population. The level of SPHK1, EDG4, EDG5, or EDG8 in a control sample, or the encoding corresponding gene copy number, is desirably typical of the general population of normal, cancer-free animals of the same species. This sample either can be collected from an animal for the purpose of being used in the methods described in the present invention or it can be any biological material representative of normal, cancer-free animals suitable for use in the methods of this invention. A control sample also can be obtained from normal tissue from the animal that has cancer or is suspected of having cancer. A "**test sample**" as used herein refers to a biological sample,

including sample of biological tissue or fluid origin, obtained, reached, or collected *in vivo*, *ex-vivo*, or *in situ*, that contains or is suspected of containing nucleic acids or polypeptides of SPHK1, EDG4, EDG5, or EDG8. A test sample also includes biological samples containing precancerous or cancer cells or tissues. Such test samples can be, but are not limited to, organs, tissues, fractions and cells isolated from mammals including, humans such as a patient, mice, and rats. A test sample also may include sections of the biological sample including tissues, for example, frozen sections taken for histologic purposes.

"Providing a biological subject, a biological sample, or a test sample" means to obtain a biological subject *in vivo*, *ex-vivo*, or *in situ*, including tissue or cell sample for use in the methods described in the present invention. Most often, this will be done by removing a sample of cells from an animal, but also can be accomplished *in vivo*, *ex-vivo*, or *in situ*, or by using previously isolated cells (for example, isolated from another person, at another time, and/or for another purpose).

"Data" includes, but is not limited to, information obtained that relates to "biological sample", "test sample", "control sample", and/or "control", as described above, wherein the information is applied in generating a test level for diagnostics, prevention, monitoring or therapeutic use. The present invention relates to methods for comparing and compiling data wherein the data is stored in electronic or paper formats. Electronic format can be selected from the group consisting of electronic mail, disk, compact disk (CD), digital versatile disk (DVD), memory card, memory chip, ROM or RAM, magnetic optical disk, tape, video, video clip, microfilm, internet, shared network, shared server and the like; wherein data is displayed, transmitted or analyzed via electronic transmission, video display, telecommunication, or by using any of the above stored formats; wherein data is compared and compiled at the site of sampling specimens or at a location where the data is transported following a process as described above.

"Overexpression" of a SPHK1, an EDG4, an EDG5, or an EDG8 gene or an "increased," or "elevated," level of a SPHK1, an EDG4, an EDG5, or an EDG8 ribonucleotide or protein refers to a level of SPHK1, EDG4, EDG5, or EDG8 ribonucleotide or polypeptide that, in

comparison with a control level of SPHK1, EDG4, EDG5, or EDG8, is detectably higher. Comparison may be carried out by statistical analyses on numeric measurements of the expression; or, it may be done through visual examination of experimental results by qualified researchers.

5 A level of SPHK1, EDG4, EDG5, or EDG8 ribonucleotide or polypeptide, that is "**expected**" in a control sample refers to a level that represents a typical, cancer-free sample, and from which an elevated, or diagnostic, presence of SPHK1, EDG4, EDG5, or EDG8 polypeptide or polynucleotide, can be distinguished. Preferably, an "expected" level will be controlled for such factors as the age, sex, medical history, *etc.* of the mammal, as well as for the particular
10 biological subject being tested.

 The phrase "**functional effects**" in the context of an assay or assays for testing compounds that modulate SPHK1, EDG4, EDG5, or EDG8 activity includes the determination of any parameter that is indirectly or directly under the influence of SPHK1, EDG4, EDG5, or EDG8, for example, a functional, physical, or chemical effect, for example, SPHK1, EDG4,
15 EDG5, or EDG8 activity, the ability to induce gene amplification or overexpression in cancer cells, and to aggravate cancer cell proliferation. "Functional effects" include *in vitro*, *in vivo*, and *ex vivo* activities.

 "**Determining the functional effect**" refers to assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of SPHK1, EDG4, EDG5,
20 or EDG8, for example, functional, physical, and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, for example, changes in spectroscopic characteristics (for example, fluorescence, absorbance, refractive index), hydrodynamic (for example, shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of SPHK1, EDG4, EDG5, or EDG8; measuring binding
25 activity or binding assays, for example, substrate binding, and measuring cellular proliferation; measuring signal transduction; or measuring cellular transformation.

 "**Inhibitors**," "**activators**," "**modulators**," and "**regulators**" refer to molecules that activate, inhibit, modulate, regulate and/or block an identified function. Any molecule having

potential to activate, inhibit, modulate, regulate and/or block an identified function can be a "test molecule," as described herein. For example, referring to oncogenic function or anti-apoptotic activity of SPHK1, EDG4, EDG5, or EDG8, such molecules may be identified using *in vitro* and *in vivo* assays of SPHK1, EDG4, EDG5, or EDG8, respectively. Inhibitors are compounds that
5 partially or totally block SPHK1, EDG4, EDG5, or EDG8 activity, respectively, decrease, prevent, or delay their activation, or desensitize their cellular response. This may be accomplished by binding to SPHK1, EDG4, EDG5, or EDG8 proteins directly or via other intermediate molecules. An antagonist or an antibody that blocks SPHK1, EDG4, EDG5, or
EDG8 activity, including inhibition of oncogenic function or anti-apoptotic activity of SPHK1,
10 EDG4, EDG5, or EDG8, respectively, is considered to be such an inhibitor. Activators are compounds that bind to SPHK1, EDG4, EDG5, or EDG8 protein directly or via other intermediate molecules, thereby increasing or enhancing their activity, stimulating or accelerating their activation, or sensitizing their cellular response. An agonist of SPHK1, EDG4,
EDG5, or EDG8 is considered to be such an activator. A modulator can be an inhibitor or
15 activator. A modulator may or may not bind SPHK1, EDG4, EDG5, or EDG8 or their protein directly; it affects or changes the activity or activation of SPHK1, EDG4, EDG5, or EDG8 or the cellular sensitivity to SPHK1, EDG4, EDG5, or EDG8, respectively. A modulator also may be a compound, for example, a small molecule, that inhibits transcription of SPHK1, EDG4, EDG5,
or EDG8 mRNA. A regulator of SPHK1, EDG4, EDG5, or EDG8 gene includes any element,
20 for example, nucleic acid, peptide, polypeptide, protein, peptide nucleic acid or the like, that influences and/or controls the transcription/expression of SPHK1, EDG4, EDG5, or EDG8 gene, respectively, or their coding region.

The group of inhibitors, activators, modulators and regulators of this invention also includes genetically modified versions of SPHK1, EDG4, EDG5, or EDG8, for example,
25 versions with altered activity. Thus, unless otherwise indicated, the group is inclusive of the naturally occurring protein as well as synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like.

"Assays for inhibitors, activators, modulators, or regulators" refer to experimental procedures including, for example, expressing SPHK1, EDG4, EDG5, or EDG8 *in vitro*, in cells, applying putative inhibitor, activator, modulator, or regulator compounds, and then determining the functional effects on SPHK1, EDG4, EDG5, or EDG8 activity or transcription, as described above. Samples that contain or are suspected of containing SPHK1, EDG4, EDG5, or EDG8 are treated with a potential activator, inhibitor, or modulator. The extent of activation, inhibition, or change is examined by comparing the activity measurement from the samples of interest to control samples. A threshold level is established to assess activation or inhibition. For example, inhibition of a SPHK1, EDG4, EDG5, or EDG8 polypeptide is considered achieved when the SPHK1, EDG4, EDG5, or EDG8 activity value relative to the control is 80% or lower. Similarly, activation of a SPHK1, EDG4, EDG5, or EDG8 polypeptide is considered achieved when the SPHK1, EDG4, EDG5, or EDG8 activity value relative to the control is two or more fold higher.

The terms **"isolated," "purified,"** or **"biologically pure"** refer to material that is free to varying degrees from components which normally accompany it as found in its native state. "Isolate" denotes a degree of separation from original source or surroundings. "Purify" denotes a degree of separation that is higher than isolation. A "purified" or "biologically pure" protein is sufficiently free of other materials such that any impurities do not materially affect the biological properties of the protein or cause other adverse consequences. That is, a nucleic acid or peptide of this invention is purified if it is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Purity and homogeneity are typically determined using analytical chemistry techniques, for example, polyacrylamide gel electrophoresis or high performance liquid chromatography. The term "purified" can denote that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. For a protein that can be subjected to modifications, for example, phosphorylation or glycosylation, different modifications may give rise to different isolated proteins, which can be separately purified. Various levels of purity may be applied as needed according to this invention in the different

methodologies set forth herein; the customary purity standards known in the art may be used if no standard is otherwise specified.

An "**isolated nucleic acid molecule**" can refer to a nucleic acid molecule, depending upon the circumstance, that is separated from the 5' and 3' coding sequences of genes or gene fragments contiguous in the naturally occurring genome of an organism. The term "isolated nucleic acid molecule" also includes nucleic acid molecules which are not naturally occurring, for example, nucleic acid molecules created by recombinant DNA techniques.

"**Nucleic acid**" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in either single- or double-stranded form. The term encompasses nucleic acids containing known nucleotide analogs or modified backbone residues or linkages, which are synthetic, naturally occurring, and non-naturally occurring, which have similar binding properties as the reference nucleic acid, and which are metabolized in a manner similar to the reference nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl phosphonates, chiral methyl phosphonates, 2-O-methyl ribonucleotides, and peptide-nucleic acids (PNAs).

Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (for example, degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with suitable mixed base and/or deoxyinosine residues (Batzer *et al.*, *Nucleic Acid Res.*, 19:081, 1991; Ohtsuka *et al.*, *J. Biol. Chem.*, 260:2600-2608, 1985; Rossolini *et al.*, *Mol. Cell Probes*, 8:91-98, 1994). The term nucleic acid can be used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

A "**host cell**" is a naturally occurring cell or a transformed cell or a transfected cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be

prokaryotic cells, for example, *E. coli*, or eukaryotic cells, for example, yeast, insect, amphibian, or mammalian cells, for example, Vero, CHO, HeLa, and others.

The term "**amino acid**" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, for example, hydroxyproline, γ -carboxyglutamate, and O-phosphoserine, phosphothreonine. "**Amino acid analogs**" refer to compounds that have the same basic chemical structure as a naturally occurring amino acid, *i.e.*, a carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, for example, homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (for example, norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. "**Amino acid mimetics**" refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that function in a manner similar to a naturally occurring amino acid. Amino acids and analogs are well known in the art.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"**Conservatively modified variants**" apply to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or similar amino acid sequences and include degenerate sequences. For example, the codons GCA, GCC, GCG and GCU all encode alanine. Thus, at every amino acid position where an alanine is specified, any of these codons can be used interchangeably in constructing a corresponding nucleotide sequence. The resulting nucleic acid variants are conservatively modified variants, since they encode the same protein (assuming that is the only alternation in the sequence). One skilled in the art recognizes that each codon in a

nucleic acid, except for AUG (sole codon for methionine) and UGG (tryptophan), can be modified conservatively to yield a functionally-identical peptide or protein molecule.

As to amino acid sequences, one skilled in the art will recognize that substitutions, deletions, or additions to a polypeptide or protein sequence which alter, add or delete a single amino acid or a small number (typically less than about ten) of amino acids is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitutions are well known in the art and include, for example, the changes of: alanine to serine; arginine to lysine; asparagine to glutamine or histidine; aspartate to glutamate; cysteine to serine; glutamine to asparagine; glutamate to aspartate; glycine to proline; histidine to asparagine or glutamine; isoleucine to leucine or valine; leucine to valine or isoleucine; lysine to arginine, glutamine, or glutamate; methionine to leucine or isoleucine; phenylalanine to tyrosine, leucine or methionine; serine to threonine; threonine to serine; tryptophan to tyrosine; tyrosine to tryptophan or phenylalanine; valine to isoleucine or leucine. Other conservative and semi-conservative substitutions are known in the art and can be employed in practice of the present invention.

The terms "**protein**", "**peptide**" and "**polypeptide**" are used herein to describe any chain of amino acids, regardless of length or post-translational modification (for example, glycosylation or phosphorylation). Thus, the terms can be used interchangeably herein to refer to a polymer of amino acid residues. The terms also apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid. Thus, the term "polypeptide" includes full-length, naturally occurring proteins as well as recombinantly or synthetically produced polypeptides that correspond to a full-length naturally occurring protein or to particular domains or portions of a naturally occurring protein. The term also encompasses mature proteins which have an added amino-terminal methionine to facilitate expression in prokaryotic cells.

The polypeptides of the invention can be chemically synthesized or synthesized by recombinant DNA methods; or, they can be purified from tissues in which they are naturally expressed, according to standard biochemical methods of purification.

Also included in the invention are "**functional polypeptides**," which possess one or more of the biological functions or activities of a protein or polypeptide of the invention. These functions or activities include the ability to bind some or all of the proteins which normally bind to SPHK1, EDG4, EDG5, or EDG8 protein.

5 The functional polypeptides may contain a primary amino acid sequence that has been modified from that considered to be the standard sequence of SPHK1, EDG4, EDG5, or EDG8 protein described herein. Preferably these modifications are conservative amino acid substitutions, as described herein.

10 A "**label**" or a "**detectable moiety**" is a composition that when linked with the nucleic acid or protein molecule of interest renders the latter detectable, via spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For example, useful labels include radioactive isotopes, magnetic beads, metallic beads, colloidal particles, fluorescent dyes, electron-dense reagents, enzymes (for example, as commonly used in an ELISA), biotin, digoxigenin, or haptens. A "**labeled nucleic acid or oligonucleotide probe**" is one that is
15 bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic bonds, van der Waals forces, electrostatic attractions, hydrophobic interactions, or hydrogen bonds, to a label such that the presence of the nucleic acid or probe may be detected by detecting the presence of the label bound to the nucleic acid or probe.

20 As used herein a "**nucleic acid or oligonucleotide probe**" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not unduly interfere with
25 hybridization. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled with isotopes, for example, chromophores, lumiphores, chromogens, or indirectly labeled with biotin

to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of a target gene of interest.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (for example, total cellular or library DNA or RNA).

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target complementary sequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and circumstance-dependent; for example, longer sequences can hybridize with specificity at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology-Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). In the context of the present invention, as used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other.

Generally, stringent conditions are selected to be about 5 to 10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (for example, 10 to 50 nucleotides) and at least about 60°C for long probes (for example, greater than 50 nucleotides). Stringent conditions

also may be achieved with the addition of destabilizing agents, for example, formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization.

Exemplary stringent hybridization conditions can be as following, for example: 50%
5 formamide, 5x SSC and 1% SDS, incubating at 42°C, or 5x SSC and 1% SDS, incubating at 65°C, with wash in 0.2x SSC and 0.1% SDS at 65°C. Alternative conditions include, for example, conditions at least as stringent as hybridization at 68°C for 20 hours, followed by washing in 2x SSC, 0.1% SDS, twice for 30 minutes at 55°C and three times for 15 minutes at 60°C. Another alternative set of conditions is hybridization in 6x SSC at about 45°C, followed
10 by one or more washes in 0.2x SSC, 0.1% SDS at 50-65°C. For PCR, a temperature of about 36°C is typical for low stringency amplification, although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and
15 specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C to 95°C for 30 sec. to 2 min., an annealing phase lasting 30 sec. to 2 min., and an extension phase of about 72°C for 1 to 2 min.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This
20 occurs, for example, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1x SSC at 45°C. A positive hybridization is at least twice
25 background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

The terms "about" or "approximately" in the context of numerical values and ranges refers to values or ranges that approximate or are close to the recited values or ranges such that

the invention can perform as intended, such as having a desired amount of nucleic acids or polypeptides in a reaction mixture, as is apparent to the skilled person from the teachings contained herein. This is due, at least in part, to the varying properties of nucleic acid compositions, age, race, gender, anatomical and physiological variations and the inexactitude of biological systems. Thus, these terms encompass values beyond those resulting from systematic error.

"**Antibody**" refers to a polypeptide comprising a framework region encoded by an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 2 kDa) and one "heavy" chain (up to about 70 kDa). Antibodies exist, for example, as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill in the art will appreciate that such fragments may be synthesized *de novo* chemically or via recombinant DNA methodologies. Thus, the term antibody, as used herein, also includes antibody fragments produced by the modification of whole antibodies, those synthesized *de novo* using recombinant DNA methodologies (for example, single chain Fv), humanized antibodies, and those identified using phage display libraries (see, for example, Knappik *et al.*, *J. Mol. Biol.*, 296:57-86, 2000; McCafferty *et al.*, *Nature*, 348:2-4, 1990), for example. For preparation of antibodies - recombinant, monoclonal, or polyclonal antibodies - any technique known in the art can be used with this invention (see, for example, Kohler and Milstein, *Nature*, 256(5517):495-497, 1975; Kozbor *et al.*, *Immunology Today*, 4:72, 1983; Cole *et al.*, pp. 77-96 in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., 1998).

Techniques for the production of single chain antibodies (See U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Transgenic mice, or other organisms, for example, other mammals, may be used to express humanized antibodies. Phage display technology also can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, for example, McCafferty *et al.*, *Nature*, 348:2-4, 1990; Marks *et al.*, *Biotechnology*, 10(7):779-783, 1992).

The term antibody is used in the broadest sense including agonist, antagonist, and blocking or neutralizing antibodies.

"Blocking antibody" is a type of antibody, as described above, that refers to a polypeptide comprising variable and framework regions encoded by an immunoglobulin gene or fragments, homologues, analogs or mimetics thereof that specifically binds and blocks biological activities of an antigen; for example, a blocking antibody to SPHK1, EDG4, EDG5, or EDG8 blocks the oncogenic function or anti-apoptotic activity of SPHK1, EDG4, EDG5, or EDG8 gene, respectively. A blocking antibody binds to critical regions of a polypeptide and thereby inhibits its function. Critical regions include protein-protein interaction sites, such as active sites, functional domains, ligand binding sites, and recognition sites. Blocking antibodies may be induced in mammals, for example in human, by repeated small injections of antigen, too small to produce strong hypersensitivity reactions. See Bellanti JA, *Immunology*, WB Saunders Co., p.131-368 (1971). Blocking antibodies can play an important role in blocking the function of a marker protein and inhibiting tumorigenic growth. See, for example, Jopling *et al.*, *J. Biol. Chem.*, 277(9):6864-73 (2002); Drebin *et al.*, *Cell*, 41(3):697-706 (1985); Drebin *et al.*, *Proc. Natl. Acad. Sci. USA*, 83(23):9129-33 (1986).

The term **"tumor-cell killing"** by anti-S1P, anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 blocking antibodies herein is meant any inhibition of tumor cell proliferation by means of blocking a function or binding to block a pathway related to tumor-cell proliferation. For example, anti-epidermal growth factor receptor monoclonal antibodies inhibit A431 tumor cell proliferation by blocking an autocrine pathway. See Mendelsohn *et al.*, *Trans Assoc Am Physicians*, 100:173-8 (1987); Masui *et al.*, *Cancer Res*, 44(3):1002-7 (1984).

The term "**S1P-, SPHK1-, EDG4-, EDG5-, or EDG8-oncogenic function-blocking antibody**" herein is meant an anti-human S1P-, SPHK1-, EDG4-, EDG5- or EDG8-antibody whose interaction with the SPHK1, EDG4, EDG5, or EDG8 protein inhibits the oncogenic function or anti-apoptotic activity of the protein mediates tumor-cell killing mechanisms, or inhibits tumor-cell proliferation. In contrast to antibodies that merely bind to tumor cells expressing SPHK1, EDG4, EDG5, or EDG8, blocking antibodies against SPHK1, EDG4, EDG5, or EDG8 mediate tumor-cell killing by mechanisms related to the oncogenic function or anti-apoptotic activity of SPHK1, EDG4, EDG5, or EDG8. See Drebin *et al.*, *Proc. Natl. Acad. Sci. USA*, 83(23):9129-33 (1986) for inhibition of tumorigenic growth; and Mendelsohn *et al.*, *Trans Assoc Am Physicians*, 100:173-8 (1987), for an example of antibody-mediated anti-proliferative activity.

An "**anti-S1P**" antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a S1P gene, mRNA, cDNA, or a subsequence thereof. Anti-S1P antibody also includes a blocking antibody that inhibits S1P activity, such as regulation of cellular proliferation and survival.. An anti-S1P antibody also can inhibit the ability of S1P to serve as a ligand for EDG family G-protein coupled receptors.

An "**anti-SPHK1**" antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a SPHK1 gene, cDNA, or a subsequence thereof. Anti-SPHK1 antibody also includes a blocking antibody that inhibits oncogenic function or anti-apoptotic activity of SPHK1 or mediates anti-proliferative activity on tumor-cell growth.

An "**anti-EDG4**" antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by an EDG4 gene, cDNA, or a subsequence thereof. Anti-EDG4 antibody also includes a blocking antibody that inhibits oncogenic function or anti-apoptotic activity of EDG4 or mediates anti-proliferative activity on tumor-cell growth.

An "**anti-EDG5**" antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by an EDG5 gene, cDNA, or a subsequence thereof. Anti-EDG5 antibody also includes a blocking antibody that inhibits oncogenic function or anti-apoptotic activity of EDG5 or mediates anti-proliferative activity on tumor-cell growth.

An "anti-EDG8" antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by an EDG8 gene, cDNA, or a subsequence thereof. Anti-EDG8 antibody also includes a blocking antibody that inhibits oncogenic function or anti-apoptotic activity of EDG8 or mediates anti-proliferative activity on tumor-cell growth.

5 "Cancer Vaccines" are substances that are designed to stimulate the immune system to launch an immune response against a specific target associated with a cancer. For a general overview on immunotherapy and vaccines for cancers, see Old L. J., *Scientific American*, September, 1996.

10 Vaccines may be preventative or therapeutic. Typically, preventative vaccines (for example, the flu vaccine) generally contain parts of polypeptides that stimulate the immune system to generate cells and/or other substances (for example, antibodies) that fight the target of the vaccines. Preventative vaccines must be given before exposure, concurrent with exposure, or shortly thereafter to the target (for example, the flu virus) in order to provide the immune system with enough time to activate and make the immune cells and substances that can attack the
15 target. Preventative vaccines stimulate an immune response that can last for years or even an individual's lifetime.

20 Therapeutic vaccines are used to combat existing disease. Thus, the goal of a therapeutic cancer vaccine is not just to prevent disease, but rather to stimulate the immune system to attack existing cancerous cells. Because of the many types of cancers and because it is often unpredictable who might get cancer, among other reasons, the cancer vaccines currently being
25 developed are therapeutic. As discussed further below, due to the difficulties associated with fighting an established cancer, most vaccines are used in combination with cytokines or adjuvants that help stimulate the immune response and/or are used in conjunction with conventional cancer therapies.

30 The immune system must be able to tolerate normal cells and to recognize and attack abnormal cells. To the immune system, a cancer cell may be different in very small ways from a normal cell. Therefore, the immune system often tolerates cancer cells rather than attacking them, which allows the cancer to grow and spread. Therefore, cancer vaccines must not only

provoke an immune response, but also stimulate the immune system strongly enough to overcome this tolerance. The most effective anti-tumor immune responses are achieved by stimulating T cells, which can recognize and kill tumor cells directly. Therefore, most current cancer vaccines try to activate T cells directly, try to enlist antigen presenting cells (APCs) to
5 activate T cells, or both. By way of example, researchers are attempting to enhance T cell activation by altering tumor cells so molecules that are normally only on APCs are now on the tumor cell, thus enabling the molecules to give T cells a stronger activating signal than the original tumor cells, and by evaluating cytokines and adjuvants to determine which are best at calling APCs to areas they are needed.

10 Cancer vaccines can be made from whole tumor cells or from substances contained by the tumor (for example, antigens). For a whole cell vaccine, tumor cells are removed from a patient(s), grown in the laboratory, and treated to ensure that they can no longer multiply and are incapable of infecting the patient. When whole tumor cells are injected into a person, an immune response against the antigens on the tumor cells is generated. There are two types of whole cell
15 cancer vaccines: 1) autologous whole cell vaccines made with a patient's own whole, inactivated tumor cells; and 2) allogenic whole cell vaccines made with another individual's whole, inactivated tumor cells (or the tumor cells from several individuals). Antigen vaccines are not made of whole cells, but of one or more antigens contained by the tumor. Some antigens are common to all cancers of a particular type, while some are unique to an individual. A few
20 antigens are shared between tumors of different types of cancer.

Antigens in an antigen vaccine may be delivered in several ways. For example, proteins or fragments thereof from the tumor cells can be given directly as the vaccine. Nucleic acids coding for those proteins can be given (for example, RNA or DNA vaccines). Furthermore, viral vectors can be engineered so that when they infect a human cell and the cell will make and
25 display the tumor antigen on its surface. The viral vector should be capable of infecting only a small number of human cells in order to start an immune response, but not enough to make a person sick. Viruses also can be engineered to make cytokines or to display proteins on their surface that help activate immune cells. These can be given alone or with a vaccine to help the

immune response. Finally, antibodies themselves may be used as antigens in a vaccine (anti-idiotypic vaccines). In this way, an antibody to a tumor antigen is administered, then the B cells make antibodies to that antibody that also recognize the tumor cells.

Cancer vaccines frequently contain components to help boost the immune response. Cytokines (for example, IL-2), which are chemical messengers that recruit other immune cells to the site of attack and help killer T cells perform their function, are frequently employed. Similarly, adjuvants, substances derived from a wide variety of sources, including bacteria, have been shown to elicit immune cells to an area where they are needed. In some cases, cytokines and adjuvants are added to the cancer vaccine mixture, in other cases they are given separately.

Cancer vaccines are most frequently developed to target tumor antigens normally expressed on the cell surface (for example, membrane-bound receptors or subparts thereof). However, cancer vaccines also may be effective against intracellular antigens that are, in a tumor-specific manner, exposed on the cell surface. Many tumor antigens are intracellular proteins that are degraded and expressed on the cell surface complexed with, for example, HLA. Frequently, it is difficult to attack these antigens with antibody therapy because they are sparsely dispersed on the cell surface. However, cancer vaccines are a viable alternative therapeutic approach.

Cancer vaccines may prove most useful in preventing cancer recurrence after surgery, radiation or chemotherapy has reduced or eliminated the primary tumor.

The term "**immunoassay**" is an assay that utilizes the binding interaction between an antibody and an antigen. Typically, an immunoassay uses the specific binding properties of a particular antibody to isolate, target, and/or quantify the antigen.

The phrase "**specifically (or selectively) binds**" to an antibody or "**specifically (or selectively) immunoreactive with**," when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bind to a particular protein at a level at least two times the background and do not

substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular protein. For example, antibodies raised to a particular SPHK1, EDG4, EDG5, or EDG8 polypeptide can be selected to obtain only those antibodies that are specifically immunoreactive with the SPHK1, EDG4, EDG5, or EDG8 polypeptide, respectively, and not with other proteins, except for polymorphic variants, orthologs, and alleles of the specific SPHK1, EDG4, EDG5, or EDG8 polypeptide. In addition, antibodies raised to a particular SPHK1, EDG4, EDG5, or EDG8 polypeptide ortholog can be selected to obtain only those antibodies that are specifically immunoreactive with the SPHK1, EDG4, EDG5, or EDG8 polypeptide ortholog, respectively, and not with other orthologous proteins, except for polymorphic variants, mutants, and alleles of the SPHK1, EDG4, EDG5, or EDG8 polypeptide ortholog. This selection may be achieved by subtracting out antibodies that cross-react with desired SPHK1, EDG4, EDG5, or EDG8 molecules, as appropriate. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein. See, for example, Harlow and Lane, *Antibodies, A Laboratory Manual*, 1988, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

The phrase "selectively associates with" refers to the ability of a nucleic acid to "selectively hybridize" with another as defined *supra*, or the ability of an antibody to "selectively (or specifically) bind" to a protein, as defined *supra*.

"siRNA" refers to small interfering RNAs, which also include short hairpin RNA (shRNA) (Paddison *et al.*, *Genes and Dev.* 16: 948-958, 2002), that are capable of causing interference and can cause post-transcriptional silencing of specific genes in cells, for example, mammalian cells (including human cells) and in the body, for example, mammalian bodies (including humans). The phenomenon of RNA interference is described and discussed in Bass, *Nature*, 411:428-29, 2001; Elbashir *et al.*, *Nature*, 411:494-98, 2001; and Fire *et al.*, *Nature*, 391:806-11, 1998, wherein methods of making interfering RNA also are discussed. The siRNAs

based upon the sequences disclosed herein (for example, GenBank Accession Nos. NM_021972, NM_004720, NM_004230, and NM_030760, for SPHK1, EDG4, EDG5, and EDG8 sequences, respectively) are typically less than 100 base pairs ("bps") in length and constituency and preferably are about 30 bps or shorter, and can be made by approaches known in the art, including the use of complementary DNA strands or synthetic approaches. The siRNAs are capable of causing interference and can cause post-transcriptional silencing of specific genes in cells, for example, mammalian cells (including human cells) and in the body, for example, mammalian bodies (including humans). Exemplary siRNAs according to the invention could have up to 30 bps, 29 bps, 25 bps, 22 bps, 21 bps, 20 bps, 15 bps, 10 bps, 5 bps or any integer thereabout or therebetween. According to the invention, siRNA having different sequences but directed against SPHK1, EDG4, EDG5, or EDG8 can be administered concurrently or consecutively in any proportion, including equimolar proportions.

The term "miRNA" refers to microRNA, a class of small RNA molecules or a small noncoding RNA molecules, that are capable of causing interference, inhibition of RNA translation into protein, and can cause post-transcriptional silencing of specific genes in cells, for example, mammalian cells (including human cells) and in the body, for example, mammalian bodies (including humans) (see, Zeng and Cullen, *RNA*, 9(1):112-123, 2003; Kidner and Martienssen *Trends Genet*, 19(1):13-6, 2003; Dennis C, *Nature*, 420(6917):732, 2002; Couzin J, *Science* 298(5602):2296-7, 2002). Previously, the miRNAs were known as small temporal RNAs (stRNAs) and belonged to a class of non-coding microRNAs, which have been shown to control gene expression either by repressing translation or by degrading the targeted mRNAs (see Couzin J, *Science* 298(5602):2296-7, 2002), which are generally 20-28 nt in length (see Finnegan *et al.*, *Curr Biol*, 13(3):236-40, 2003; Ambros *et al.*, *RNA* 9(3):277-279, 2003; Couzin J, *Science* 298(5602):2296-7, 2002). Unlike other RNAs (for example, siRNAs or shRNAs), miRNAs or stRNAs are not encoded by any microgenes, but are generated from aberrant (probably double-stranded) RNAs by an enzyme called *Dicer*, which cleaves double-stranded RNA into smaller pieces (see Couzin J, *Science* 298(5602):2296-7, 2002). According to the invention, miRNA having different sequences but directed against SPHK1, EDG4, EDG5, or

EDG8 can be administered concurrently or consecutively in any proportion, including equimolar proportions.

The term "**transgene**" refers to a nucleic acid sequence encoding, for example, one of the SPHK1, EDG4, EDG5, or EDG8 polypeptides, or an antisense transcript thereto, which is partly or entirely heterologous, *i.e.*, foreign, to the transgenic organism or cell into which it is introduced, or, is homologous to an endogenous gene of the transgenic animal or cell into which it is introduced, but which is designed to be inserted, or is inserted, into the animal's genome in such a way as to alter the genome of the cell into which it is inserted (for example, it is inserted at a location which differs from that of the natural gene or its insertion results in a knockout). A transgene can include one or more transcriptional regulatory sequences and any other nucleic acid, (for example, an intron), that may be necessary for optimal expression of a selected nucleic acid.

By "**transgenic**" is meant any organism that includes a nucleic acid sequence, which is inserted into a cell and becomes a part of the genome of the animal that develops from that cell.

Such a transgene may be partly or entirely heterologous to the transgenic animal.

Thus, for example, substitution of the naturally occurring SPHK1, EDG4, EDG5, or EDG8 gene for a gene from a second species results in an animal that produces the protein of the second species. Substitution of the naturally occurring gene for a gene having a mutation results in an animal that produces the mutated protein. A transgenic mouse, see below, expressing the human SPHK1, EDG4, EDG5, or EDG8 protein can be generated by direct replacement of the mouse SPHK1, EDG4, EDG5, or EDG8 subunit with the human gene. These transgenic animals can be critical for drug antagonist studies on animal models for human diseases, and for eventual treatment of disorders or diseases associated with the respective genes. Transgenic mice carrying these mutations will be extremely useful in studying this disease.

A "**transgenic animal**" refers to any animal, preferably a non-human mammal, that is chimeric, and is achievable with most vertebrate species. Such species include, but are not limited to, non-human mammals, including rodents, for example, mice and rats; rabbits; birds or amphibians; ovines, for example, sheep and goats; porcines, for example, pigs; and bovines, for

example, cattle and buffalo; in which one or more of the cells of the animal contains heterologous nucleic acid introduced by way of human intervention, for example, by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of the cell, by way of deliberate genetic manipulation, for example, by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or sexual fertilization, but rather is directed to the introduction of a recombinant DNA molecule. This molecule may be integrated within a chromosome, or it may be extrachromosomally replicating DNA. In the typical transgenic animals described herein, the transgene causes cells to express a recombinant form of one of the SPHK1, EDG4, EDG5, or EDG8 proteins, for example, either agonistic or antagonistic forms. However, transgenic animals in which the recombinant SPHK1, EDG4, EDG5, or EDG8 gene is silent also are contemplated. Moreover, "transgenic animal" also includes those recombinant animals in which gene disruption of one or more SPHK1, EDG4, EDG5, or EDG8 gene is caused by human intervention, including both recombination and antisense techniques. The transgene can be limited to somatic cells or be placed into the germline.

Methods of obtaining transgenic animals are described in, for example, Puhler, A., Ed., *Genetic Engineering of Animals*, VCH Pub., 1993; Murphy and Carter, Eds., *Transgenesis Techniques: Principles and Protocols (Methods in Molecular Biology, Vol. 18)*, 1993; and Pinkert, CA, Ed., *Transgenic Animal Technology: A Laboratory Handbook*, Academic Press, 1994.

The term "**knockout construct**" refers to a nucleotide sequence that is designed to decrease or suppress expression of a polypeptide encoded by an endogenous gene in one or more cells of a mammal. The nucleotide sequence used as the knockout construct is typically comprised of (1) DNA from some portion of the endogenous gene (one or more exon sequences, intron sequences, and/or promoter sequences) to be suppressed and (2) a marker sequence used to detect the presence of the knockout construct in the cell. The knockout construct can be inserted into a cell containing the endogenous gene to be knocked out. The knockout construct

can then integrate with one or both alleles of an endogenous gene, for example, SPHK1, EDG4, EDG5, or EDG8 gene, and such integration of the knockout construct can prevent or interrupt transcription of the full-length endogenous gene. Integration of the knockout construct into the cellular chromosomal DNA is typically accomplished via homologous recombination (*i.e.*, regions of the knockout construct that are homologous or complementary to endogenous DNA sequences can hybridize to each other when the knockout construct is inserted into the cell; these regions can then recombine so that the knockout construct is incorporated into the corresponding position of the endogenous DNA).

A transgenic animal carrying a "**knockout**" of SPHK1, EDG4, EDG5, or EDG8 gene, would be useful for the establishment of a non-human model for diseases involving such proteins, and to distinguish between the activities of the different SPHK1, EDG4, EDG5, or EDG8 proteins in an *in vivo* system. "**Knockout mice**" refers to mice whose native or endogenous SPHK1, EDG4, EDG5, or EDG8 allele or alleles have been disrupted by homologous recombination or the like and which produce no functional SPHK1, EDG4, EDG5, or EDG8 of their own. Knockout mice may be produced in accordance with techniques known in the art, for example, Thomas, *et al.*, *Immunol*, 163:978-84, 1999; Kanakaraj, *et al.*, *J Exp Med*, 187:2073-9, 1998; or Yeh *et al.*, *Immunity*, 7:715-725, 1997.

"**Aptamers**": An aptamer is a peptide, a peptide-like, a nucleic acid, or a nucleic acid-like molecule that is capable of binding to a specific molecule (for example, SPHK1, EDG4, EDG5, or EDG8) of interest with high affinity and specificity. An aptamer also can be a peptide or a nucleic acid molecule that mimics the three dimensional structure of active portions of the peptides or the nucleic acid molecules of the invention. (see, for example, James W., *Current Opinion in Pharmacology*, 1:540-546 (2001); Colas *et al.*, *Nature* 380:548-550 (1996); Tuerk and Gold, *Science* 249:505 (1990); Ellington and Szostak, *Nature* 346:818 (1990)). The specific binding molecule of the invention may be a chemical mimetic; for example, a synthetic peptide aptamer or peptidomimetic. It is preferably a short oligomer selected for binding affinity and bioavailability (for example, passage across the plasma and nuclear membranes, resistance to hydrolysis of oligomeric linkages, adsorbance into cellular tissue, and resistance to metabolic

breakdown). The chemical mimetic may be chemically synthesized with at least one non-natural analog of a nucleoside or amino acid (for example, modified base or ribose, designer or non-classical amino acid, D or L optical isomer). Modification also may take the form of acylation, glycosylation, methylation, phosphorylation, sulfation, or combinations thereof. Oligomeric linkages may be phosphodiester or peptide bonds; linkages comprised of a phosphorus, nitrogen, sulfur, oxygen, or carbon atom (for example, phosphorothionate, disulfide, lactam, or lactone bond); or combinations thereof. The chemical mimetic may have significant secondary structure (for example, a ribozyme) or be constrained (for example, a cyclic peptide).

"Peptide Aptamer": A peptide aptamer is a polypeptide or a polypeptide-like molecule that is capable of binding to a specific molecule (for example, SPHK1 and/or EDG4 and/or EDG5 and/or EDG8) of interest with high affinity and specificity. A peptide aptamer also can be a polypeptide molecule that mimics the three dimensional structure of active portions of the polypeptide molecules of the invention. A peptide-aptamer can be designed to mimic the recognition function of complementarity determining regions of immunoglobulins, for example. The aptamer can recognize different epitopes on the protein surface (for example, SPHK1 and/or EDG4 and/or EDG5 and/or EDG8) with dissociation equilibrium constants in the nanomolar range; those inhibit the protein (for example, SPHK1 and/or EDG4 and/or EDG5 and/or EDG8) activity. Peptide aptamers are analogous to monoclonal antibodies, with the advantages that they can be isolated together with their coding genes, that their small size facilitates solution of their structures, and that they can be designed to function inside cells.

An peptide aptamer is typically between about 3 and about 100 amino acids or the like in length. More commonly, an aptamer is between about 10 and about 35 amino acids or the like in length. Peptide-aptamers may be prepared by any known method, including synthetic, recombinant, and purification methods (James W., *Current Opinion in Pharmacology*, 1:540-546 (2001); Colas *et al.*, *Nature* 380:548-550 (1996)).

The instant invention also provides aptamers of SPHK1, EDG4, EDG5, and EDG8 peptides. In one aspect, the invention provides aptamers of isolated polypeptides comprising at least one active fragment having substantially homologous sequence of SPHK1, EDG4, EDG5,

or EDG8 peptides (for example, SEQ ID NO:2, SEQ ID NO:5, SEQ ID NO:7, or SEQ ID NO:9, respectively, or any fragment thereof). The instant aptamers are peptide molecules that are capable of binding to a protein or other molecule, or mimic the three dimensional structure of the active portion of the peptides of the invention.

5 **"Nucleic Acid Aptamer"**: A nucleic acid aptamer is a nucleic acid or a nucleic acid-like molecule that is capable of binding to a specific molecule (for example, SPHK1 and/or EDG4 and/or EDG5 and/or EDG8) of interest with high affinity and specificity. A nucleic acid aptamer also can be a nucleic acid molecule that mimics the three dimensional structure of active portions of the nucleic acid molecules of the invention. A nucleic acid-aptamer is typically between
10 about 9 and about 300 nucleotides or the like in length. More commonly, an aptamer is between about 30 and about 100 nucleotides or the like in length. Nucleic acid-aptamers may be prepared by any known method, including synthetic, recombinant, and purification methods (James W., *Current Opinion in Pharmacology*, 1:540-546 (2001); Colas *et al.*, *Nature* 380:548-550 (1996)).

 According to one aspect of the invention, aptamers of the instant invention include non-
15 modified or chemically modified RNA, DNA, PNA or polynucleotides. The method of selection may be by, but is not limited to, affinity chromatography and the method of amplification by reverse transcription (RT) or polymerase chain reaction (PCR). Aptamers have specific binding regions which are capable of forming complexes with an intended target molecule in an environment wherein other substances in the same environment are not complexed to the nucleic
20 acid.

 The instant invention also provides aptamers of SPHK1, EDG4, EDG5, and EDG8 polynucleotides. In another aspect, the invention provides aptamers of isolated polynucleotides comprising at least one active fragment having substantially homologous sequence of SPHK1, EDG4, EDG5, or EDG8 polynucleotides (for example, SEQ ID NO:1, SEQ ID NO:3, SEQ ID
25 NO:4, SEQ ID NO:6, SEQ ID NO:8 or SEQ ID NO:10, or any fragment thereof). The instant aptamers are nucleic acid molecules that are capable of binding to a nucleic acid or other molecule, or mimic the three dimensional structure of the active portion of the nucleic acids of the invention.

The invention also provides nucleic acids (for example, mRNA molecules) that include an aptamer as well as a coding region for a regulatory polypeptide. The aptamer is positioned in the nucleic acid molecule such that binding of a ligand to the aptamer prevents translation of the regulatory polypeptide.

5 "**SPHK1**": The term "SPHK1" can refer to SPHK1 nucleic acid (DNA and RNA) or protein (or polypeptide), and can include their polymorphic variants, alleles, mutants, and interspecies homologs that have (i) substantial nucleotide sequence homology (for example, at least 60% identity, preferably at least 70% sequence identity, more preferably at least 80%, still more preferably at least 90% and even more preferably at least 95%) with the nucleotide
10 sequence of the GenBank Accession No. NM_021972 (GenBank Protein ID. NP_068807.2), *Homo sapiens* Sphingosine kinase 1 (SPHK1) (Accession No. for *Homo sapiens* SPHK1: NM_021972; PID g21361088); or (ii) at least 65% sequence homology with the amino acid sequence of the GenBank Protein ID. NP_068807.2 (SPHK1); or (iii) substantial nucleotide
15 sequence homology (for example, at least 60% identity, preferably at least 70% sequence identity, more preferably at least 80%, still more preferably at least 90% and even more preferably at least 95%) with the nucleotide sequence as set forth in SEQ ID NO:1 or SEQ ID NO:3; or (iv) substantial sequence homology with the encoded amino acid sequence (for example, SEQ ID NO:2).

SPHK1 polynucleotides or polypeptides are typically from a mammal including, but not
20 limited to, human, rat, mouse, hamster, cow, pig, horse, sheep, or any mammal. A " SPHK1 polynucleotide" and a " SPHK1 polypeptide," may be either naturally occurring, recombinant, or synthetic (for example, *via* chemical synthesis).

SPHK1 DNA sequence, GenBank Accession No. NM_021972, contains about 1869 base pairs (see SEQ ID NO:1), which includes a coding sequence of about 1197 base pairs (see SEQ
25 ID NO:3), encoding a protein, GenBank Protein ID. NP_068807.2, of approximately 398 amino acids (see SEQ ID NO:2).

According to an aspect of the present invention, it has been determined that SPHK1 is amplified and/or overexpressed in human cancers, including colon cancer, ovarian cancer, brain

cancer, breast cancer, lung cancer, and bladder cancer. Human chromosome region 17q25 is one of the most frequently amplified regions in human cancers including colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, and bladder cancer.

More than one gene is located in this region. In a process of characterizing one of the
5 17q25.2 amplicons, SPHK1 was found amplified in human breast cancer, colon cancer, lung cancer, brain cancer, ovarian cancer and other tumor samples. Studies have shown that such amplification is usually associated with aggressive histologic types. Therefore, amplification of tumor-promoting gene(s) located on 17q25.2 can play an important role in the development and/or progression of cancers including primary colon cancer, ovarian cancer, brain cancer,
10 breast cancer, lung cancer, or bladder cancer, particularly those of the invasive histology.

Amplification of SPHK1 was determined via microarray analysis. See, for example, US Patent No. 6,232,068; Pollack *et al.*, *Nat. Genet.* 23(1):41-46, (1999) and other approaches known in the art. Amplified cell lines or tumors (for example, colon, ovary, brain, breast, lung, or bladder) were examined for DNA copy number of nearby genes and DNA sequences that map
15 to the boundaries of the amplified regions. Further analysis provided evidence that SPHK1 gene is present at the epicenter.

SPHK1 was found to be amplified in 20% (5/24) of breast cancer cell lines and 17% (15/88) of primary breast tumors. SPHK1 was found amplified in 21% (4/19) of ovarian tumors, 33% (3/9) of bladder tumors, 6% (2/35) of colon tumors, and 3% (1/30) lung tumors (see *infra*
20 Table 1). SPHK1 was found to be overexpressed in 30% (4/12) of breast cancer cell lines and 31% (17/54) of primary breast tumors. The amplification and overexpression in the same tumor sample correlated well in the sense that overexpression was observed in the amplified samples and, in addition, overexpression was observed in samples without genomic amplification (see *infra* Table 2). The folds of amplification and folds of overexpression were measured by
25 TaqMan and RT-TaqMan, respectively, using SPHK1-specific fluorogenic TaqMan probes.

"**EDG4**": The term "EDG4" can refer to EDG4 nucleic acid (DNA and RNA) or protein (or polypeptide), and can include their polymorphic variants, alleles, mutants, and interspecies homologs that have (i) substantial nucleotide sequence homology (for example, at least 60%

identity, preferably at least 70% sequence identity, more preferably at least 80%, still more preferably at least 90% and even more preferably at least 95%) with the nucleotide sequence of the GenBank Accession No. NM_004720 (GenBank Protein ID. NP_004711.2), *Homo sapiens* endothelial differentiation gene, lysophosphatidic acid G-protein-coupled receptor, 4 (EDG4) (Accession No. for *Homo sapiens* EDG4: NM_004720); or (ii) at least 65% sequence homology with the amino acid sequence of the GenBank Protein ID. NP_004711.2 (EDG4); or (iii) substantial nucleotide sequence homology (for example, at least 60% identity, preferably at least 70% sequence identity, more preferably at least 80%, still more preferably at least 90% and even more preferably at least 95%) with the nucleotide sequence as set forth in SEQ ID NO:4; or (iv) substantial sequence homology with the encoded amino acid sequence (for example, SEQ ID NO:5).

EDG4 polynucleotides or polypeptides are typically from a mammal including, but not limited to, human, rat, mouse, hamster, cow, pig, horse, sheep, or any mammal. An "EDG4 polynucleotide" and an "EDG4 polypeptide," may be either naturally occurring, recombinant, or synthetic (for example, *via* chemical synthesis).

EDG4 DNA sequence contains 1056 base pairs (see SEQ ID NO:4), encoding a protein of 351 amino acids (see SEQ ID NO:5).

According to an aspect of the present invention, it has been determined that EDG4 is amplified and/or overexpressed in human cancers, including breast cancer, colon cancer, lung cancer, ovarian cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, and esophagus cancer. Human chromosome region 19p12 is one of the most frequently amplified regions in human cancers including breast cancer, colon cancer, lung cancer, ovarian cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, and esophagus cancer.

More than one gene is located in this region. In a process of characterizing one of the 19p12 amplicons, EDG4 was found amplified in human breast, colon, lung, ovarian, liver, kidney, head and neck, stomach, esophagus and other tumor samples (see Figure 1). Studies have shown that such amplification is usually associated with aggressive histologic types. Therefore, amplification of tumor-promoting gene(s) located on 19p12 can play an important

role in the development and/or progression of cancers including primary breast cancer, colon cancer, lung cancer, ovarian cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, and particularly those of the invasive histology.

Amplification of EDG4 was determined via microarray analysis. See, for example, US Patent No. 6,232,068; Pollack *et al.*, *Nat. Genet.* 23(1):41-46, (1999) and other approaches known in the art. Amplified tumors (for example, breast, colon, lung, ovary, liver, kidney, head and neck, stomach, or esophagus) were examined for DNA copy number of nearby genes and DNA sequences that map to the boundaries of the amplified regions. TaqMan epicenter data for EDG4 is shown in Figure 3. Further analysis provided evidence that EDG4 gene is present at the epicenter.

EDG4 was found to be amplified and/or overexpressed in human breast, colon, lung, ovarian, liver, stomach, head and neck, esophagus, or kidney tumors (see *infra* Figures 1, 2, and Table 3). EDG4 was found to be amplified in over 10% (6/58) of human breast tumors, over 11% (11/99) of human colon tumors, over 25% (20/78) of human lung tumors, 6% (2/34) of human ovarian tumors, over 17% (6/35) of human head and neck tumors, over 13% (5/38) of human liver tumors, 29% (15/52) of human kidney tumors, over 22% (8/36) of human stomach tumors, and 12% (5/42) of human esophagus tumors (see Figure 1). EDG4 was found to be overexpressed in over 12% (6/47) of human breast tumors, over 17% (6/35) of human colon tumors, over 1% (1/78) of human lung tumors, over 19% (6/31) of human ovarian tumors, over 3% (1/28) of human head and neck tumors, 26% (8/31) of human liver tumors, and over 22% (7/31) of human kidney tumors (see Figure 2). The folds of amplification and folds of overexpression were measured by TaqMan and RT-TaqMan, respectively, using EDG4-specific fluorogenic TaqMan probes.

"EDG5": The term "EDG5" can refer to EDG5 nucleic acid (DNA and RNA) or protein (or polypeptide), and can include their polymorphic variants, alleles, mutants, and interspecies homologs that have (i) substantial nucleotide sequence homology (for example, at least 60% identity, preferably at least 70% sequence identity, more preferably at least 80%, still more preferably at least 90% and even more preferably at least 95%) with the nucleotide sequence of

the GenBank Accession No. NM_004230 (GenBank Protein ID. NP_004221.1), *Homo sapiens* endothelial differentiation gene, sphingolipid G-protein-coupled receptor, 5 (EDG5) (Accession No. for *Homo sapiens* EDG5: NM_004230); or (ii) at least 65% sequence homology with the amino acid sequence of the GenBank Protein ID. NP_004221.1 (EDG5); or (iii) substantial
5 nucleotide sequence homology (for example, at least 60% identity, preferably at least 70% sequence identity, more preferably at least 80%, still more preferably at least 90% and even more preferably at least 95%) with the nucleotide sequence as set forth in SEQ ID NO:6; or (iv) substantial sequence homology with the encoded amino acid sequence (for example, SEQ ID NO:7).

10 EDG5 polynucleotides or polypeptides are typically from a mammal including, but not limited to, human, rat, mouse, hamster, cow, pig, horse, sheep, or any mammal. An "EDG5 polynucleotide" and an "EDG5 polypeptide," may be either naturally occurring, recombinant, or synthetic (for example, *via* chemical synthesis).

EDG5 DNA sequence contains 1062 base pairs (see SEQ ID NO:6), encoding a protein
15 of 353 amino acids (see SEQ ID NO:7).

According to an aspect of the present invention, it has been determined that EDG5 is amplified and/or overexpressed in human cancers, including colon cancer, breast cancer, lung cancer, liver cancer, or bladder cancer. Human chromosome region 19p13.3 is one of the most frequently amplified regions in human cancers including colon cancer, breast cancer, lung
20 cancer, liver cancer, and bladder cancer.

More than one gene is located in this region. In a process of characterizing one of the 19p13.3 amplicons, EDG5 was found amplified in human colon, breast, lung, liver, bladder, and other tumor samples. Studies have shown that such amplification is usually associated with aggressive histologic types. Therefore, amplification of tumor-promoting gene(s) located on
25 19p13.3 can play an important role in the development and/or progression of cancers including primary colon cancer, breast cancer, lung cancer, liver cancer, or bladder cancer, particularly those of the invasive histology.

Amplification of EDG5 was determined via microarray analysis. See, for example, US Patent No. 6,232,068; Pollack *et al.*, *Nat. Genet.* 23(1):41-46, (1999) and other approaches known in the art. Amplified tumors (for example, colon, breast, lung, liver or bladder) were examined for DNA copy number of nearby genes and DNA sequences that map to the boundaries of the amplified regions. TaqMan epicenter data for EDG5 is shown in Figure 4. Further analysis provided evidence that EDG5 gene is present at the epicenter.

EDG5 was found to be amplified in 20% (8/40) of human lung tumors, 21% (21/100) of human breast tumors, 23% (8/35) of human colon tumors, 10% (2/19) of human liver tumors, and over 22% (2/9) of human bladder tumors (see *infra* Table 4). The folds of amplification and folds of overexpression were measured by TaqMan and RT-TaqMan, respectively, using EDG5-specific fluorogenic TaqMan probes.

"EDG8": The term "EDG8" can refer to EDG8 nucleic acid (DNA and RNA) or protein (or polypeptide), and can include their polymorphic variants, alleles, mutants, and interspecies homologs that have (i) substantial nucleotide sequence homology (for example, at least 60% identity, preferably at least 70% sequence identity, more preferably at least 80%, still more preferably at least 90% and even more preferably at least 95%) with the nucleotide sequence of the GenBank Accession No. NM_030760 (GenBank Protein ID. NP_110387.1), *Homo sapiens* endothelial differentiation gene, sphingolipid G-protein-coupled receptor, 8 (EDG8) (Accession No. for *Homo sapiens* EDG8: NM_030760); or (ii) at least 65% sequence homology with the amino acid sequence of the GenBank Protein ID. NP_110387.1 (EDG8); or (iii) substantial nucleotide sequence homology (for example, at least 60% identity, preferably at least 70% sequence identity, more preferably at least 80%, still more preferably at least 90% and even more preferably at least 95%) with the nucleotide sequence as set forth in SEQ ID NO:8, SEQ ID NO: 10; or (iv) substantial sequence homology with the encoded amino acid sequence (for example, SEQ ID NO:9).

EDG8 polynucleotides or polypeptides are typically from a mammal including, but not limited to, human, rat, mouse, hamster, cow, pig, horse, sheep, or any mammal. An "EDG8

polynucleotide" and an "EDG8 polypeptide," may be either naturally occurring, recombinant, or synthetic (for example, *via* chemical synthesis).

EDG8 DNA sequence, GenBank Accession No. NM_030760, contains 2306 base pairs (see SEQ ID NO:8), which includes a coding sequence of about 1197 base pairs (see SEQ ID NO:10), encoding a protein, GenBank Protein ID. NP_110387.1, of approximately 398 amino acids (see SEQ ID NO:9).

According to an aspect of the present invention, it has been determined that EDG8 is amplified and/or overexpressed in human cancers, including colon cancer, breast cancer, and lung cancer. Human chromosome region 19p13.3 is one of the most frequently amplified regions in human cancers including colon cancer, breast cancer, lung cancer, liver cancer, and bladder cancer.

More than one gene is located in this region. In a process of characterizing one of the 19p13.3 amplicons, EDG8 was found amplified in human colon, breast, lung, liver, bladder, and other tumor samples. Studies have shown that such amplification is usually associated with aggressive histologic types. Therefore, amplification of tumor-promoting gene(s) located on 19p13.3 can play an important role in the development and/or progression of cancers including primary colon cancer, breast cancer, lung cancer, liver cancer, or bladder cancer, particularly those of the invasive histology.

Amplification of EDG8 was determined via microarray analysis. See, for example, US Patent No. 6,232,068; Pollack *et al.*, *Nat. Genet.* 23(1):41-46, (1999) and other approaches known in the art. Amplified cell lines or tumors (for example, colon, breast, lung, liver or bladder) were examined for DNA copy number of nearby genes and DNA sequences that map to the boundaries of the amplified regions. TaqMan epicenter data for EDG8 is shown in Figure 4. Further analysis provided evidence that EDG8 gene is present at the epicenter.

EDG8 was found to be amplified in 17% (5/30) of human lung tumors, 10% (10/100) of human breast tumors, 26% (9/35) of human colon tumors, 10% (2/19) of human liver tumors and over 22% (2/9) of human bladder tumors (see *infra* Table 5). EDG8 was found to be

overexpressed in over 68% (13/19) of colon tumors, over 73% (14/19) of breast tumors, and over 31% (6/19) of lung tumors tested (see *infra* Table 5). The folds of amplification and folds of overexpression were measured by TaqMan and RT-TaqMan, respectively, using EDG8-specific fluorogenic TaqMan probes.

5

More details on the role of SPHK1, EDG4, EDG5, and EDG8 in tumorigenesis are discussed in the sections below.

2. Amplification of SPHK1, EDG4, EDG5, and EDG8 Genes in Tumors:

10 The presence of a target gene that has undergone amplification in tumors is evaluated by determining the copy number of the target genes, *i.e.*, the number of DNA sequences in a cell encoding the target protein. Generally, a normal diploid cell has two copies of a given autosomal gene. The copy number can be increased, however, by gene amplification or duplication, for example, in cancer cells, or reduced by deletion. Methods of evaluating the copy number of a
15 particular gene are well known in the art, and include, *inter alia*, hybridization and amplification based assays.

Any of a number of hybridization based assays can be used to detect the copy number of the SPHK1, EDG4, EDG5, or EDG8 genes in the cells of a biological subject. One such method is Southern blot (see Ausubel *et al.*, or Sambrook *et al.*, *supra*), where the genomic DNA is
20 typically fragmented, separated electrophoretically, transferred to a membrane, and subsequently hybridized to a SPHK1, EDG4, EDG5, or EDG8 specific probe. Comparison of the intensity of the hybridization signal from the probe for the target region with a signal from a control probe from a region of normal nonamplified, single-copied genomic DNA in the same genome provides an estimate of the relative SPHK1, EDG4, EDG5, or EDG8 copy number,
25 corresponding to the specific probe used. An increased signal compared to control represents the presence of amplification.

A methodology for determining the copy number of the SPHK1, EDG4, EDG5, or EDG8 gene in a sample is *in situ* hybridization, for example, fluorescence *in situ* hybridization (FISH) (see Angerer, 1987 *Meth. Enzymol.*, 152: 649). Generally, *in situ* hybridization comprises the following major steps: (1) fixation of tissue or biological structure to be analyzed; (2) prehybridization treatment of the biological structure to increase accessibility of target DNA, and to reduce nonspecific binding; (3) hybridization of the mixture of nucleic acids to the nucleic acid in the biological structure or tissue; (4) post-hybridization washes to remove nucleic acid fragments not bound in the hybridization, and (5) detection of the hybridized nucleic acid fragments. The probes used in such applications are typically labeled, for example, with radioisotopes or fluorescent reporters. Preferred probes are sufficiently long, for example, from about 50, 100, or 200 nucleotides to about 1000 or more nucleotides, to enable specific hybridization with the target nucleic acid(s) under stringent conditions.

Another alternative methodology for determining number of DNA copies is comparative genomic hybridization (CGH). In comparative genomic hybridization methods, a "test" collection of nucleic acids is labeled with a first label, while a second collection (for example, from a normal cell or tissue) is labeled with a second label. The ratio of hybridization of the nucleic acids is determined by the ratio of the first and second labels binding to each fiber in an array. Differences in the ratio of the signals from the two labels, for example, due to gene amplification in the test collection, is detected and the ratio provides a measure of the SPHK1, EDG4, EDG5, or EDG8 gene copy number, corresponding to the specific probe used. A cytogenetic representation of DNA copy-number variation can be generated by CGH, which provides fluorescence ratios along the length of chromosomes from differentially labeled test and reference genomic DNAs.

Hybridization protocols suitable for use with the methods of the invention are described, for example, in Albertson (1984) *EMBO J.* 3:1227-1234; Pinkel (1988) *Proc. Natl. Acad. Sci. USA*, 85:9138-9142; *EPO Pub. No. 430:402*; *Methods in Molecular Biology*, Vol. 33: *In Situ Hybridization Protocols*, Choo, ed., Humana Press, Totowa, NJ (1994).

Amplification-based assays also can be used to measure the copy number of the SPHK1, EDG4, EDG5, or EDG8 gene. In such assays, the corresponding SPHK1, EDG4, EDG5, or EDG8 nucleic acid sequence act as a template in an amplification reaction (for example, Polymerase Chain Reaction or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the copy number of the SPHK1, EDG4, EDG5, or EDG8 gene, corresponding to the specific probe used, according to the principles discussed above. Methods of real-time quantitative PCR using TaqMan probes are well known in the art. Detailed protocols for real-time quantitative PCR are provided, for example, for RNA in: Gibson *et al.*, 1996, A novel method for real time quantitative RT-PCR. *Genome Res.*, 10:995-1001; and for DNA in: Heid *et al.*, 1996, Real time quantitative PCR. *Genome Res.*, 10:986-994.

A TaqMan-based assay also can be used to quantify SPHK1, EDG4, EDG5, or EDG8 polynucleotides. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, for example, AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, for example, <http://www2.perkin-elmer.com>).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see, Wu and Wallace, *Genomics*, 4: 560, 1989; Landegren *et al.*, *Science*, 241: 1077, 1988; and Barringer *et al.*, *Gene*, 89:117, 1990), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA*, 86:1173, 1989), self-sustained sequence replication (Guatelli *et al.*, *Proc. Natl. Acad. Sci. USA* 87:1874, 1990), dot PCR, and linker adapter PCR, for example.

One powerful method for determining DNA copy numbers uses microarray-based platforms. Microarray technology may be used because it offers high resolution. For example, the traditional CGH generally has a 20 Mb limited mapping resolution; whereas in microarray-

based CGH, the fluorescence ratios of the differentially labeled test and reference genomic DNAs provide a locus-by-locus measure of DNA copy-number variation, thereby achieving increased mapping resolution. Details of various microarray methods can be found in the literature. See, for example, US Patent No. 6,232,068; Pollack *et al.*, *Nat. Genet.*, 23(1):41-6, (1999), and others.

As demonstrated in the Examples set forth herein, the SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 gene is frequently amplified in certain cancers, particularly colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, and bladder cancer. As described herein, results showing cells exhibiting a SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 DNA copy number increase also demonstrate SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 mRNA overexpression, respectively. The SPHK1, EDG4, EDG5, and EDG8 genes have the characteristic features of overexpression, amplification, and the correlation between these two has been established in several tumor types. These features are shared with other well-studied oncogenes (Yoshimoto *et al.*, *JPN J Cancer Res*, 77(6):540-5, 1986; Knuutila *et al.*, *Am. J. Pathol.*, 152(5):1107-23, 1998). The SPHK1, EDG4, EDG5, and EDG8 genes and the encoded polypeptides are accordingly used in the present invention as targets for cancer diagnosis, prevention, and treatment.

3. Frequent Overexpression of SPHK1, EDG4, EDG5, and EDG8 Genes in Tumors:

The expression levels of the SPHK1, EDG4, EDG5, and EDG8 genes in tumors cells were examined. As demonstrated in the examples *infra*, SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 gene(s) is/are overexpressed in cancers, including colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, and bladder cancer. Detection and quantification of the SPHK1, EDG4, EDG5, or EDG8 gene expression may be carried out through direct hybridization based assays or amplification based assays. The hybridization based techniques for measuring gene transcript are known to those skilled in the art (Sambrook *et al.*, *Molecular*

Cloning: A Laboratory Manual, 2d Ed. vol. 1-3, Cold Spring Harbor Press, NY, 1989). For example, one method for evaluating the presence, absence, or quantity of the SPHK1, EDG4, EDG5, or EDG8 gene is by Northern blot. Isolated mRNAs from a given biological subject are electrophoresed to separate the mRNA species, and transferred from the gel to a membrane, for example, a nitrocellulose or nylon filter. Labeled SPHK1, EDG4, EDG5, or EDG8 probes are then hybridized to the membrane to identify and quantify the respective mRNAs. The example of amplification based assays include RT-PCR, which is well known in the art (Ausubel *et al.*, *Current Protocols in Molecular Biology*, eds. 1995 supplement). Quantitative RT-PCR is used preferably to allow the numerical comparison of the level of respective SPHK1, EDG4, EDG5, or EDG8 mRNAs in different samples. Other assays, such as Northern hybridization or microarray analysis also can be used to determine the numerical comparison of respective mRNA levels.

4. Cancer Diagnosis, Therapies, and Vaccines Using SPHK1, EDG4, EDG5, and EDG8:

A. **Overexpression and Amplification of the SPHK1, EDG4, EDG5, and EDG8 Genes:**

The SPHK1, EDG4, EDG5, and EDG8 genes and their expressed gene products can be used for diagnosis, prognosis, rational drug design, and other therapeutic intervention of tumors and cancers (for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer).

Detection and measurement of amplification and/or overexpression of the SPHK1, EDG4, EDG5, or EDG8 gene in a test sample taken from a patient indicates that the patient may have developed a tumor. Particularly, the presence of amplified SPHK1, EDG4, EDG5, or EDG8 DNA leads to a diagnosis of cancer or precancerous condition, for example, a colon cancer, an ovarian cancer, a brain cancer, a breast cancer, a lung cancer, a liver cancer, a kidney

cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or a bladder cancer, with high probability of accuracy. The present invention therefore provides, in one aspect, methods for diagnosing or characterizing a cancer or tumor in a mammalian tissue by measuring the levels of SPHK1, EDG4, EDG5, or EDG8 mRNA expression in samples taken from the tissue of suspicion, and determining whether SPHK1, EDG4, EDG5, or EDG8 is overexpressed in the tissue. The various techniques, including hybridization-, microarray-, and amplification-based methods, for measuring and evaluating mRNA levels are provided herein as discussed *supra*. The present invention also provides, in other aspects, methods for diagnosing a cancer or tumor in a mammalian tissue by measuring the numbers of SPHK1, EDG4, EDG5, or EDG8 DNA copy in samples taken from the tissue of suspicion, and determining whether the SPHK1, EDG4, EDG5, or EDG8 gene is amplified in the tissue. The various techniques, including hybridization based and amplification based methods, for measuring and evaluating DNA copy numbers are provided herein as discussed *supra*. The present invention thus provides methods for detecting amplified genes at the DNA level and increased expression at the RNA level, wherein both the results are indicative of tumor progression.

B. Detection of the SPHK1, EDG4, EDG5, and EDG8 Proteins:

According to the present invention, the detection of increased SPHK1, EDG4, EDG5, or EDG8 protein level in a test sample also can indicate the presence of a precancerous or cancerous condition in the tissue source of the sample. Protein detection for tumor and cancer diagnostics and prognostics can be carried out by immunoassays, for example, using antibodies directed against a target gene, for example, SPHK1, EDG4, EDG5, or EDG8. Any methods that are known in the art for protein detection and quantitation can be used in the methods of this invention, including, *inter alia*, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, immunoelectrophoresis, radioimmunoassay (RIA), enzyme-linked immunosorbent assays (ELISAs), immuno-flouorescent assays, Western Blot, *etc.* Protein from the tissue or cell type to be analyzed may be isolated using standard techniques, for example, as

described in Harlow and Lane, *Antibodies: A Laboratory Manual* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. 1988).

The antibodies (or fragments thereof) useful in the present invention can, additionally, be employed histologically, as in immunofluorescence or immunoelectron microscopy, for *in situ* detection of target gene peptides. *In situ* detection can be accomplished by removing a histological specimen from a patient, and applying thereto a labeled antibody of the present invention. The antibody (or its fragment) is preferably applied by overlaying the labeled antibody (or fragment) onto a biological sample. Through the use of such a procedure, it is possible to determine not only the presence of the target gene product, for example, SPHK1, EDG4, EDG5, or EDG8 protein, but also its distribution in the examined tissue. Using the present invention, a skilled artisan will readily perceive that any of a wide variety of histological methods (for example, staining procedures) can be modified to achieve such *in situ* detection.

The biological sample that is subjected to protein detection can be brought in contact with and immobilized on a solid phase support or carrier, for example, nitrocellulose, or other solid support which is capable of immobilizing cells, cell particles, or soluble proteins. The support can then be washed with suitable buffers followed by treatment with the detectably labeled fingerprint gene specific antibody. The solid phase support can then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on the solid support can then be detected by conventional means.

A target gene product-specific antibody, for example, a SPHK1, EDG4, EDG5, or EDG8 antibody can be detectably labeled, in one aspect, by linking the same to an enzyme, for example, horseradish peroxidase, alkaline phosphatase, or glucoamylase, and using it in an enzyme immunoassay (EIA) (see, for example, Voller, A., 1978, The Enzyme Linked Immunosorbent Assay (ELISA), *Diagnostic Horizons*, 2:1-7; Voller *et al.*, *J. Clin. Pathol.*, 31:507-520, 1978; Butler, J. E., *Meth. Enzymol.*, 73:482-523, 1981; Maggio, E. (ed.), *Enzyme Immunoassay*, CRC Press, Boca Raton, Fla., 1980; and Ishikawa *et al.* (eds), *Enzyme Immunoassay*, Kigaku Shoin, Tokyo, 1981). The enzyme bound to the antibody reacts with an appropriate substrate, preferably a chromogenic substrate, in such a manner as to produce a

chemical moiety that can be detected, for example, by spectrophotometric or fluorimetric means, or by visual inspection.

In a related aspect, therefore, the present invention provides the use of SPHK1, EDG4, EDG5, or EDG8 antibodies in cancer diagnosis and intervention. Antibodies that specifically
5 bind to SPHK1, EDG4, EDG5, or EDG8 protein and polypeptides can be produced by a variety of methods. Such antibodies may include, but are not limited to, polyclonal antibodies, monoclonal antibodies (mAbs), humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab')₂ fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies, and epitope-binding fragments of any of the above.

10 Such antibodies can be used, for example, in the detection of the target gene, SPHK1, EDG4, EDG5, or EDG8, or its fingerprint or pathway genes involved in a particular biological pathway, which may be of physiological or pathological importance. These potential pathways or fingerprint genes, for example, may interact with SPHK1, EDG4, EDG5, or EDG8 activity and be involved in tumorigenesis. The SPHK1, EDG4, EDG5, or EDG8 antibodies also can be
15 used in a method for the inhibition of SPHK1, EDG4, EDG5, or EDG8 activity, respectively. Thus, such antibodies can be used in treating tumors and cancers (for example, colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, a head and neck cancer, a stomach cancer, an esophagus cancer, or bladder cancer); they also may be used in diagnostic procedures whereby patients are tested for abnormal levels of SPHK1, EDG4,
20 EDG5, or EDG8 protein, and/or fingerprint or pathway gene product associated with SPHK1, EDG4, EDG5, or EDG8, respectively, and for the presence of abnormal forms of such protein.

To produce antibodies to SPHK1, EDG4, EDG5, or EDG8 protein, a host animal is immunized with the protein, or a portion thereof. Such host animals can include, but are not limited to, rabbits, mice, and rats. Various adjuvants can be used to increase the immunological
25 response, depending on the host species, including but not limited to Freund's (complete and incomplete), mineral gels, for example, aluminum hydroxide, surface active substances, for example, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet

hemocyanin (KLH), dinitrophenol (DNP), and potentially useful human adjuvants, for example, BCG (*Bacille Calmette-Guerin*) and *Corynebacterium parvum*.

Monoclonal antibodies, which are homogeneous populations of antibodies to a particular antigen, for example, SPHK1, EDG4, EDG5, or EDG8 as in the present invention, can be
5 obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to the hybridoma technique of Kohler and Milstein, (*Nature*, 256:495-497, 1975; and U.S. Pat. No. 4,376,110), the human B-cell hybridoma technique (Kosbor *et al.*, *Immunology Today*, 4:72, 1983; Cole *et al.*, *Proc. Natl. Acad. Sci. USA*, 80:2026-2030, 1983), and the BV-hybridoma technique (Cole *et al.*, *Monoclonal*
10 *Antibodies And Cancer Therapy* (Alan R. Liss, Inc. 1985), pp. 77-96. Such antibodies can be of any immunoglobulin class including IgG, IgM, IgE, IgA, IgD and any subclass thereof. The hybridoma producing the mAb of this invention can be cultivated *in vitro* or *in vivo*. Production of high titers of mAbs *in vivo* makes this the presently preferred method of production.

In addition, techniques developed for the production of "chimeric antibodies" can be
15 made by splicing the genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity (see, Morrison *et al.*, *Proc. Natl. Acad. Sci. USA*, 81:6851-6855, 1984; Neuberger *et al.*, *Nature*, 312:604-608, 1984; Takeda *et al.*, *Nature*, 314:452-454, 1985; and U.S. Pat. No. 4,816,567). A chimeric antibody is a molecule in which different portions are derived from different animal
20 species, for example, those having a variable region derived from a murine mAb and a container region derived from human immunoglobulin.

Alternatively, techniques described for the production of single chain antibodies (for example, U.S. Pat. No. 4,946,778; Bird, *Science*, 242:423-426, 1988; Huston *et al.*, *Proc. Natl. Acad. Sci. USA*, 85:5879-5883, 1988; and Ward *et al.*, *Nature*, 334:544-546, 1989), and for
25 making humanized monoclonal antibodies (U.S. Pat. No. 5,225,539), can be used to produce anti-differentially expressed or anti-pathway gene product antibodies.

Knappik *et al.* (see U.S. Pat. No. 6,300,064) describe methods for generating antibody libraries of human-derived antibody genes, which cover the antibodies encoded in the human

genome. The methods disclosed also enable creation of useful libraries of (poly)peptides in general.

Antibody fragments that recognize specific epitopes can be generated by known techniques. For example, such fragments include but are not limited to: the F(ab')₂ fragments that can be produced by pepsin digestion of the antibody molecule, and the Fab fragments that can be generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries can be constructed (Huse *et al.*, *Science*, 246:1275-1281, 1989) to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity.

C. Use of SPHK1, EDG4, EDG5, and EDG8 Modulators in Cancer Diagnostics:

In addition to antibodies, the present invention provides, in another aspect, the diagnostic and therapeutic utilities of other molecules and compounds that interact with SPHK1, EDG4, EDG5, or EDG8 protein. Specifically, such compounds can include, but are not limited to proteins or peptides, comprising extracellular portions of transmembrane proteins of the target, if they exist. Exemplary peptides include soluble peptides, for example, Ig-tailed fusion peptides. Such compounds also can be obtained through the generation and screening of random peptide libraries (see, for example, Lam *et al.*, *Nature*, 354:82-84, 1991; Houghton *et al.*, *Nature*, 354:84-86, 1991), made of D- and/or L-configuration amino acids, phosphopeptides (including, but not limited to, members of random or partially degenerate phosphopeptide libraries; see, for example, Songyang *et al.*, *Cell*, 72:767-778, 1993), and small organic or inorganic molecules. In this aspect, the present invention provides a number of methods and procedures to assay or identify compounds that bind to target, *i.e.*, SPHK1, EDG4, EDG5, or EDG8 protein, or to any cellular protein that may interact with the target, and compounds that may interfere with the interaction of the target with other cellular proteins.

In vitro assay systems are provided that are capable of identifying compounds that specifically bind to the target gene product, for example, SPHK1, EDG4, EDG5, or EDG8 protein. The assays involve, for example, preparation of a reaction mixture of the target gene

product, for example, SPHK1, EDG4, EDG5, or EDG8 protein and a test compound under conditions and for a time sufficient to allow the two components to interact and bind, thus forming a complex that can be removed and/or detected in the reaction mixture. These assays can be conducted in a variety of ways. For example, one method involves anchoring the target protein or the test substance to a solid phase, and detecting target protein – test compound complexes anchored to the solid phase at the end of the reaction. In one aspect of such a method, the target protein can be anchored onto a solid surface, and the test compound, which is not anchored, can be labeled, either directly or indirectly. In practice, microtiter plates can be used as the solid phase. The anchored component can be immobilized by non-covalent or covalent attachments. Non-covalent attachment can be accomplished by simply coating the solid surface with a solution of the protein and drying. Alternatively, an immobilized antibody, preferably a monoclonal antibody, specific for the protein to be immobilized can be used to anchor the protein to the solid surface. The surfaces can be prepared in advance and stored.

To conduct the assay, the non-immobilized component is added to the coated surface containing the anchored component. After the reaction is complete, unreacted components are removed, for example, by washing, and complexes anchored on the solid surface are detected. Where the previously immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the previously non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; for example, using a labeled antibody specific for the immobilized component (the antibody, in turn, can be directly labeled or indirectly labeled with a labeled anti-Ig antibody). Alternatively, the reaction can be conducted in a liquid phase, the reaction products separated from unreacted components, and complexes detected, for example, using an immobilized antibody specific for a target gene or the test compound to anchor any complexes formed in solution, and a labeled antibody specific for the other component of the possible complex to detect anchored complexes.

Assays also are provided for identifying any cellular protein that may interact with the target protein, *i.e.*, SPHK1, EDG4, EDG5, or EDG8 protein. Any method suitable for detecting

protein-protein interactions can be used to identify novel interactions between target protein and cellular or extracellular proteins. Those cellular or extracellular proteins may be involved in certain cancers, for example, colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, or bladder cancer, and represent certain tumorigenic pathways including the target, for example, SPHK1, EDG4, EDG5, or EDG8. They may thus be denoted as pathway genes.

Methods, for example, co-immunoprecipitation and co-purification through gradients or chromatographic columns, can be used to identify protein-protein interactions engaged by the target protein. The amino acid sequence of the target protein, *i.e.*, SPHK1, EDG4, EDG5, or EDG8 protein or a portion thereof, is useful in identifying the pathway gene products or other proteins that interact with SPHK1, EDG4, EDG5, or EDG8 protein. The amino acid sequence of pathway gene products or other proteins can be derived from the nucleotide sequence, or from published database records (SWISS-PROT, PIR, EMBL); it also can be ascertained using techniques well known to a skilled artisan, for example, the Edman degradation technique (see, for example, Creighton, *Proteins: Structures and Molecular Principles*, 1983, W. H. Freeman & Co., N.Y., 34-49). The nucleotide subsequences of the target gene, for example, SPHK1, EDG4, EDG5, or EDG8, can be used in a reaction mixture to screen for pathway gene sequences. Screening can be accomplished, for example, by standard hybridization or PCR techniques. Techniques for the generation of oligonucleotide mixtures and the screening are well known (see, for example, Ausubel, *supra*, and Innis *et al.* (eds.), *PCR Protocols: A Guide to Methods and Applications*, 1990, Academic Press, Inc., New York).

By way of example, the yeast two-hybrid system which is often used in detecting protein interactions *in vivo* is discussed herein. Chien *et al.* has reported the use of a version of the yeast two-hybrid system (*Proc. Natl. Acad. Sci. USA*, 1991, 88:9578-9582); it is commercially available from Clontech (Palo Alto, CA). Briefly, utilizing such a system, plasmids are constructed that encode two hybrid proteins: the first hybrid protein comprises the DNA-binding domain of a transcription factor, for example, activation protein, fused to a known protein, in this case, a protein known to be involved in a tumor or cancer, and the second hybrid protein

comprises the transcription factor's activation domain fused to an unknown protein that is encoded by a cDNA which has been recombined into this plasmid as part of a cDNA library. The plasmids are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene, for example, *lacZ*, whose expression is regulated by the transcription factor's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. The DNA binding hybrid protein cannot activate transcription because it does not provide the activation domain function, and the activation domain hybrid protein cannot activate transcription because it lacks the domain required for binding to its target site, *i.e.*, it cannot localize to the transcription activator protein's binding site. Interaction between the DNA binding hybrid protein and the library encoded protein reconstitutes the functional transcription factor and results in expression of the reporter gene, which is detected by an assay for the reporter gene product.

The two-hybrid system or similar methods can be used to screen activation domain libraries for proteins that interact with a known "bait" gene product. The SPHK1, EDG4, EDG5, or EDG8 gene product, involved in a number of tumors and cancers, is such a bait according to the present invention. Total genomic or cDNA sequences are fused to the DNA encoding an activation domain. This library and a plasmid encoding a hybrid of the bait gene product, *i.e.*, SPHK1, EDG4, EDG5, or EDG8 protein or polypeptides, fused to the DNA-binding domain are co-transformed into a yeast reporter strain, and the resulting transformants are screened for those that express the reporter gene. For example, the bait gene SPHK1, EDG4, EDG5, or EDG8 can be cloned into a vector such that it is translationally fused to the DNA encoding the DNA-binding domain of the GAL4 protein. The colonies are purified and the plasmids responsible for reporter gene expression are isolated. The inserts in the plasmids are sequenced to identify the proteins encoded by the cDNA or genomic DNA.

A cDNA library of a cell or tissue source that expresses proteins predicted to interact with the bait gene product, for example, SPHK1, EDG4, EDG5, or EDG8, can be made using methods routinely practiced in the art. According to the particular system described herein, the library is generated by inserting the cDNA fragments into a vector such that they are

translationally fused to the activation domain of GAL4. This library can be cotransformed along with the bait gene-GAL4 fusion plasmid into a yeast strain which contains a *lacZ* gene whose expression is controlled by a promoter which contains a GAL4 activation sequence. A cDNA encoded protein, fused to GAL4 activation domain, that interacts with the bait gene product will
5 reconstitute an active GAL4 transcription factor and thereby drive expression of the *lacZ* gene. Colonies that express *lacZ* can be detected by their blue color in the presence of X-gal. Plasmids from such a blue colony can then be purified and used to produce and isolate the SPHK1-, EDG4-, EDG5-, or EDG8-interacting protein using techniques routinely practiced in the art.

The assay systems involve, for example, preparation of a reaction mixture containing the
10 target gene product SPHK1, EDG4, EDG5, or EDG8 protein, and the binding partner under conditions and for a time sufficient to allow the two products to interact and bind, thus forming a complex. To test a compound for inhibitory activity, the reaction mixture is prepared in the presence and absence of the test compound. The test compound can be initially included in the reaction mixture, or can be added at a time subsequent to the addition of a target gene product
15 and its cellular or extracellular binding partner. Control reaction mixtures are incubated without the test compound or with a placebo. The formation of complexes between the target gene product SPHK1, EDG4, EDG5, or EDG8 protein and the cellular or extracellular binding partner is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction
20 of the target gene product SPHK1, EDG4, EDG5, or EDG8 protein and the interactive binding partner. Additionally, complex formation within reaction mixtures containing the test compound and normal target gene product can be compared to complex formation within reaction mixtures containing the test compound and mutant target gene product. This comparison can be important in the situation where it is desirable to identify compounds that disrupt interactions of mutant but
25 not normal target gene product.

The assays can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the target gene product SPHK1, EDG4, EDG5, or EDG8 protein or the binding partner to a solid phase and detecting complexes anchored to the solid phase at the

end of the reaction, as described above. In homogeneous assays, the entire reaction is carried out in a liquid phase, as described below. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the target gene product SPHK1, EDG4, EDG5, or EDG8 protein and the binding partners, for example, by competition, can be identified by conducting the reaction in the presence of the test substance; *i.e.*, by adding the test substance to the reaction mixture prior to or simultaneously with the target gene product SPHK1, EDG4, EDG5, or EDG8 protein and interactive cellular or extracellular binding partner. Alternatively, test compounds that disrupt preformed complexes, for example, compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed.

In a homogeneous assay, a preformed complex of the target gene product and the interactive cellular or extracellular binding partner product is prepared in which either the target gene products or their binding partners are labeled, but the signal generated by the label is quenched due to complex formation (see, for example, Rubenstein, U.S. Pat. No. 4,109,496). The addition of a test substance that competes with and displaces one of the species from the preformed complex will result in the generation of a signal above background. The test substances that disrupt the interaction between the target gene product SPHK1, EDG4, EDG5, or EDG8 protein and cellular or extracellular binding partners can thus be identified.

In one aspect, the target gene product SPHK1, EDG4, EDG5, or EDG8 protein can be prepared for immobilization using recombinant DNA techniques. For example, the target SPHK1, EDG4, EDG5, or EDG8 coding region can be fused to a glutathione-S-transferase (GST) gene using a fusion vector, for example, pGEX-5X-1, in such a manner that its binding activity is maintained in the resulting fusion product. The interactive cellular or extracellular binding partner product is purified and used to raise a monoclonal antibody, using methods routinely practiced in the art. This antibody can be labeled with the radioactive isotope ^{125}I , for example, by methods routinely practiced in the art.

In a heterogeneous assay, the GST-Target gene fusion product is anchored, for example, to glutathione-agarose beads. The interactive cellular or extracellular binding partner is then added in the presence or absence of the test compound in a manner that allows interaction and binding to occur. At the end of the reaction period, unbound material is washed away, and the
5 labeled monoclonal antibody can be added to the system and allowed to bind to the complexed components. The interaction between the target gene product SPHK1, EDG4, EDG5, or EDG8 protein and the interactive cellular or extracellular binding partner is detected by measuring the corresponding amount of radioactivity that remains associated with the glutathione-agarose beads. A successful inhibition of the interaction by the test compound will result in a decrease in
10 measured radioactivity. Alternatively, the GST-target gene fusion product and the interactive cellular or extracellular binding partner can be mixed together in liquid in the absence of the solid glutathione-agarose beads. The test compound is added either during or after the binding partners are allowed to interact. This mixture is then added to the glutathione-agarose beads and unbound material is washed away. Again, the extent of inhibition of the binding partner
15 interaction can be detected by adding the labeled antibody and measuring the radioactivity associated with the beads.

In other aspects of the invention, these same techniques are employed using peptide fragments that correspond to the binding domains of the target gene product, for example, SPHK1, EDG4, EDG5, or EDG8 protein and the interactive cellular or extracellular binding
20 partner (where the binding partner is a product), in place of one or both of the full-length products. Any number of methods routinely practiced in the art can be used to identify and isolate the protein's binding site. These methods include, but are not limited to, mutagenesis of one of the genes encoding one of the products and screening for disruption of binding in a co-immunoprecipitation assay.

25 Additionally, compensating mutations in the gene encoding the second species in the complex can be selected. Sequence analysis of the genes encoding the respective products will reveal mutations that correspond to the region of the product involved in interactive binding. Alternatively, one product can be anchored to a solid surface using methods described above,

and allowed to interact with and bind to its labeled binding partner, which has been treated with a proteolytic enzyme, for example, trypsin. After washing, a short, labeled peptide comprising the binding domain can remain associated with the solid material, which can be isolated and identified by amino acid sequencing. Also, once the gene coding for the cellular or extracellular binding partner product is obtained, short gene segments can be engineered to express peptide fragments of the product, which can then be tested for binding activity and purified or synthesized.

D. Methods for Cancer Treatment Using SPHK1, EDG4, EDG5, and EDG8 Modulators:

In another aspect, the present invention provides methods for treating or controlling a cancer or tumor and the symptoms associated therewith. Any compounds, for example, those identified in the aforementioned assay systems, can be tested for the ability to prevent and/or ameliorate symptoms of tumors and cancers (for example, colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, or bladder cancer). As used herein, inhibit, control, ameliorate, prevent, treat, and suppress collectively and interchangeably mean stopping or slowing cancer formation, development, or growth and/or eliminating or reducing cancer symptoms. Cell-based and animal model-based trial systems for evaluating the ability of the tested compounds to prevent and/or ameliorate tumors and cancer symptoms are used according to the present invention.

For example, cell based systems can be exposed to a compound suspected of ameliorating colon, ovarian, brain, breast, lung, liver, kidney, or bladder tumor or cancer symptoms, at a sufficient concentration and for a time sufficient to elicit such an amelioration in the exposed populations of cells. After exposure, the populations of cells are examined to determine whether one or more tumor / cancer phenotypes represented in the populations has been altered to resemble a more normal or more wild-type, non-cancerous phenotype. Further, the levels of SPHK1, EDG4, EDG5, or EDG8 mRNA expression and DNA amplification within these cells

may be determined, according to the methods provided herein. A decrease in the observed level of expression and amplification would indicate the successful intervention of tumors and cancers (for example, colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, or bladder cancer).

5 In addition, animal models can be used to identify compounds for use as drugs and pharmaceuticals that are capable of treating or suppressing symptoms of tumors and cancers. For example, animal models can be exposed to a test compound at a sufficient concentration and for a time sufficient to elicit such an amelioration in the exposed animals. The response of the animals to the exposure can be monitored by assessing the reversal of symptoms associated with
10 the tumor or cancer, or by evaluating the changes in DNA copy number in cell populations and levels of mRNA expression of the target gene, for example, SPHK1, EDG4, EDG5, or EDG8. Any treatments which reverse any symptom of tumors and cancers, and/or which reduce overexpression and amplification of the target SPHK1, EDG4, EDG5, or EDG8 gene may be considered as candidates for therapy in humans. Dosages of test agents can be determined by
15 deriving dose-response curves.

 Moreover, fingerprint patterns or gene expression profiles can be characterized for known cell states, for example, normal or known pre-neoplastic, neoplastic, or metastatic states, within the cell- and/or animal-based model systems. Subsequently, these known fingerprint patterns can be compared to ascertain the ability of a test compound to modify such fingerprint patterns,
20 and to cause the pattern to more closely resemble that of a normal fingerprint pattern. For example, administration of a compound which interacts with and affects SPHK1, EDG4, EDG5, or EDG8 gene expression and amplification or cells overexpressing or having amplification may cause the fingerprint pattern of a precancerous or cancerous model system to more closely resemble a control, normal system; such a compound thus will have therapeutic utilities in
25 treating the cancer. In other situations, administration of a compound may cause the fingerprint pattern of a control system to begin to mimic tumors and cancers (for example, colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, or bladder cancer); such a compound therefore

acts as a tumorigenic agent, which in turn can serve as a target for therapeutic interventions of the cancer and its diagnosis.

In another aspect, the present invention also provides assays for compounds that interfere with gene and cellular protein interactions involving the target SPHK1, EDG4, EDG5, or EDG8.

5 The target gene product, for example, SPHK1, EDG4, EDG5, or EDG8 protein, may interact *in vivo* with one or more cellular or extracellular macromolecules, for example, proteins and nucleic acid molecules. Such cellular and extracellular macromolecules are referred to as "binding partners." Compounds that disrupt such interactions can be used to regulate the activity of the target gene product, for example, SPHK1, EDG4, EDG5, or EDG8 protein, especially
10 mutant target gene product. Such compounds can include, but are not limited to, molecules, for example, antibodies, peptides and other chemical compounds.

E. Methods for Identifying Small Molecules That Can be Used as SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 Modulators:

15 As described herein, the modulators contemplated by the present invention can be small organic compounds. Such modulators can be identified by assays (for example, in microtiter formats on microtiter plates in robotic assays) used to screen large numbers of compounds. There are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka Chemika-Biochemica Analytika (Buchs
20 Switzerland) and the like.

In particular, modulators displaying a desired activity can be identified from combinatorial libraries (*i.e.*, collections of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of "building blocks"). Preparation and screening of combinatorial libraries is well known to those of skill in the art.
25 Such combinatorial libraries include, but are not limited to, peptide libraries (see, for example, U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.* 37:487-493 (1991) and Houghton *et al.*, *Nature* 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries also can

be used. Such chemistries include, but are not limited to: peptoids (see, for example, PCT Publication No. WO 91/19735), encoded peptides (*e.g.*, PCT Publication WO 93/20242), random bio-oligomers (*e.g.*, PCT Publication No. WO 92/00091), benzodiazepines (see, for example, U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *Proc. Nat. Acad. Sci. USA* 90:6909-6913 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.* 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.* 114:9217-9218 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.* 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science* 261:1303 (1993)), and/or peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.* 59:658 (1994)), nucleic acid libraries (see, for example, Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (see, for example, U.S. Patent 5,539,083), antibody libraries (see, for example, Vaughn *et al.*, *Nature Biotechnology*, 14(3):309-314 (1996) and PCT/US96/10287), carbohydrate libraries (*see, e.g.*, Liang *et al.*, *Science*, 274:1520-1522 (1996) and U.S. Patent 5,593,853), small organic molecule libraries (see, for example, benzodiazepines, Baum C&EN, Jan 18, page 33 (1993); isoprenoids, U.S. Patent 5,569,588; thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pyrrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, for example, 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA). In addition, numerous combinatorial libraries are commercially available (see, for example, ComGenex, Princeton, N.J., Tripos, Inc., St. Louis, MO, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

High-throughput assays also can be used to identify the modulators. Using the high-throughput assays, it is possible to screen thousands of potential modulators in a single day. For example, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10

wells can test a single modulator. Thus, a single standard microtiter plate can assay about 100 (for example, 96) modulators. If 1536 well plates are used, then a single plate easily can assay from about 100- about 1500 different compounds.

5 **F. Methods for Monitoring Efficacy of Cancer Treatment:**

In one aspect, the present invention provides methods for monitoring the efficacy of a therapeutic treatment regimen of cancer and methods for monitoring the efficacy of a compound in clinical trials or other research studies for inhibition of tumors. The monitoring can be accomplished by detecting and measuring, in the biological samples taken from a patient at
10 various time points during the course of the application of a treatment regimen for treating a cancer or a clinical trial or other research studies, the changed levels of expression or amplification of the target gene, for example, SPHK1, EDG4, EDG5, or EDG8 in the cell population or sample. A level of expression and/or amplification that is lower in samples taken at the later time of the treatment or trial or a research study than those at the earlier time indicates
15 that the treatment regimen is effective to control the cancer in the patient, or the compound is effective in inhibiting the tumor. In contrast, samples taken at the later time of the treatment or trial or a research study showing no statistically significant decrease in level of expression and/or amplification than those at the earlier time indicates that the treatment regimen is not effective to control the cancer in the patient, or the compound is not effective in inhibiting the tumor. Of
20 course, the time course studies should be so designed that sufficient time is allowed for the treatment regimen or the compound to exert any effect it may have.

Therefore, the influence of compounds on tumors and cancers can be monitored both in a clinical trial or other research studies and in a basic drug screening. In a clinical trial or other research studies, for example, tumor cells can be isolated from colon, ovarian, brain, breast, lung,
25 liver, kidney, or bladder tumor removed by surgery, and RNA prepared and analyzed by Northern blot analysis or TaqMan RT-PCR as described herein, or alternatively by measuring the amount of protein produced. The fingerprint expression profiles thus generated can serve as putative biomarkers for colon, ovarian, brain, breast, lung, liver, kidney, or bladder tumor or

cancer. Particularly, the expression of SPHK1, EDG4, EDG5, or EDG8 serves as one such biomarker. Thus, by monitoring the level of expression of the differentially or over-expressed genes, for example, SPHK1, EDG4, EDG5, or EDG8, an effective treatment protocol can be developed using suitable chemotherapeutic anticancer drugs.

5

G. Use of Additional Modulators to SPHK1, EDG4, EDG5, or EDG8 Nucleotides in Cancer Treatment:

In another further aspect of this invention, additional compounds and methods for treatment of tumors are provided. Symptoms of tumors and cancers can be controlled by, for example, target gene modulation, and/or by a depletion of the precancerous or cancerous cells. Target gene modulation can be of a negative or positive nature, depending on whether the target resembles a gene (for example, tumorigenic) or a tumor suppressor gene (for example, tumor suppressive). That is, inhibition, *i.e.*, a negative modulation, of an oncogene-like target gene or stimulation, *i.e.*, a positive modulation, of a tumor suppressor-like target gene will control or ameliorate the tumor or cancer in which the target gene is involved. More precisely, "negative modulation" refers to a reduction in the level and/or activity of target gene or its product, for example, SPHK1, EDG4, EDG5, or EDG8, relative to the level and/or activity of the target gene or its product in the absence of the modulatory treatment. "Positive modulation" refers to an increase in the level and/or activity of target gene or its product, for example, SPHK1, EDG4, EDG5, or EDG8, relative to the level and/or activity of target gene or its product in the absence of modulatory treatment. Particularly because SPHK1, EDG4, EDG5, or EDG8 shares many features with well known oncogenes as discussed *supra*, inhibition of the SPHK1, EDG4, EDG5, or EDG8 gene, their protein, or their activities will control or ameliorate precancerous or cancerous conditions, for example, colon cancer and/or ovarian cancer and/or brain cancer and/or breast cancer and/or lung cancer and/or liver cancer and/or kidney cancer and/or bladder cancer.

The techniques to inhibit or suppress a target gene, for example SPHK1, EDG4, EDG5, or EDG8, that are involved in cancer are provided in the present invention. Such approaches include negative modulatory techniques. For example, compounds that exhibit negative

modulatory activity on SPHK1, EDG4, EDG5, or EDG8 can be used in accordance with the invention to prevent and/or ameliorate symptoms of tumors and cancers (for example, colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, or bladder cancer). Such molecules can include, but are not limited to, peptides, phosphopeptides, small molecules (molecular weight below about 500 Daltons), large molecules (molecular weight above about 500 Daltons), or antibodies (including, for example, polyclonal, monoclonal, humanized, anti-idiotypic, chimeric or single chain antibodies, and Fab, F(ab')₂ and Fab expression library fragments, and epitope-binding fragments thereof), and nucleic acid molecules that interfere with replication, transcription, or translation of the SPHK1, EDG4, EDG5, or EDG8 gene (for example, antisense RNA, Antisense DNA, DNA decoy or decoy molecule, siRNAs, miRNA, triple helix forming molecules, and ribozymes, which can be administered in any combination).

Antisense, siRNAs, miRNAs, and ribozyme molecules that inhibit expression of a target gene, for example, SPHK1, EDG4, EDG5, or EDG8, can be used to reduce the level of the functional activities of the target gene and its product, for example, reduce the catalytic potency of SPHK1, EDG4, EDG5, or EDG8, respectively. Triple helix forming molecules can be used in reducing the level of target gene activity. These molecules can be designed to reduce or inhibit either wild type, or if appropriate, mutant target gene activity.

For example, anti-sense RNA and DNA molecules act to directly block the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. With respect to antisense DNA or DNA decoy, oligodeoxyribonucleotides derived from the translation initiation site, for example, between the -10 and +10 regions of the target gene nucleotide sequence of interest, are preferred.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. A review is provided in Rossi, *Current Biology*, 4:469-471 (1994). The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by an endonucleolytic cleavage. A composition of ribozyme molecules must include one or more sequences complementary to the target gene

mRNA, and must include a well-known catalytic sequence responsible for mRNA cleavage (U.S. Pat. No. 5,093,246). Engineered hammerhead motif ribozyme molecules that may specifically and efficiently catalyze internal cleavage of RNA sequences encoding target protein, for example, SPHK1, EDG4, EDG5, or EDG8, may be used according to this invention in cancer
5 intervention.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the molecule of interest, for example, SPHK1, EDG4, EDG5, or EDG8 RNA, for ribozyme cleavage sites which include the following sequences, GUA, GUU and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the
10 region of the target gene, for example, SPHK1, EDG4, EDG5, or EDG8, containing the cleavage site can be evaluated for predicted structural features, for example, secondary structure, that can render an oligonucleotide sequence unsuitable. The suitability of candidate sequences also can be evaluated by testing their accessibility to hybridization with complementary oligonucleotides, using ribonuclease protection assays.

The SPHK1, EDG4, EDG5, and EDG8 gene sequences also can be employed in an RNA
15 interference context. The phenomenon of RNA interference is described and discussed in Bass, *Nature*, 411: 428-29 (2001); Elbashir *et al.*, *Nature*, 411: 494-98 (2001); and Fire *et al.*, *Nature*, 391: 806-11 (1998), where methods of making interfering RNA also are discussed. The double-stranded RNA based upon the sequence disclosed herein (for example, GenBank Accession No.
20 NM_021972, NM_004720, NM_004230, and NM_030760 for SPHK1, EDG4, EDG5, and EDG8, respectively) is typically less than 100 base pairs ("bps") in length and constituency and preferably is about 30 bps or shorter, and can be made by approaches known in the art, including the use of complementary DNA strands or synthetic approaches. The RNAs that are capable of causing interference can be referred to as small interfering RNAs (siRNAs), small hairpin RNAs
25 (shRNAs), or microRNAs (miRNAs), and can cause post-transcriptional silencing of specific genes in cells, for example, mammalian cells (including human cells) and in the body, for example, mammalian bodies (including humans). Exemplary siRNAs according to the invention

could have up to 30 bps, 29 bps, 25 bps, 22 bps, 21 bps, 20 bps, 15 bps, 10 bps, 5 bps or any number thereabout or therebetween.

5 Nucleic acid molecules that can associate together in a triple-stranded conformation (triple helix) and that thereby can be used to inhibit transcription of a target gene, should be single helices composed of deoxynucleotides. The base composition of these oligonucleotides must be designed to promote triple helix formation via Hoogsteen base pairing rules, which generally require sizeable stretches of either purines or pyrimidines on one strand of a duplex. Nucleotide sequences can be pyrimidine-based, which will result in TAT and CGC triplets across the three associated strands of the resulting triple helix. The pyrimidine-rich molecules provide
10 bases complementary to a purine-rich region of a single strand of the duplex in a parallel orientation to that strand. In addition, nucleic acid molecules can be chosen that are purine-rich, for example, those that contain a stretch of G residues. These molecules will form a triple helix with a DNA duplex that is rich in GC pairs, in which the majority of the purine residues are located on a single strand of the targeted duplex, resulting in GGC triplets across the three
15 strands in the triplex. Alternatively, the potential sequences that can be targeted for triple helix formation can be increased by creating a so-called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair first with one strand of a duplex and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines on one strand of a duplex.

20 In instances wherein the antisense, ribozyme, siRNA, miRNA, and triple helix molecules described herein are used to reduce or inhibit mutant gene expression, it is possible that they also can effectively reduce or inhibit the transcription (for example, using a triple helix) and/or translation (for example, using antisense or ribozyme molecules) of mRNA produced by the normal target gene allele. These situations are pertinent to tumor suppressor genes whose
25 normal levels in the cell or tissue need to be maintained while a mutant is being inhibited. To do this, nucleic acid molecules which are resistant to inhibition by any antisense, ribozyme or triple helix molecules used, and which encode and express target gene polypeptides that exhibit normal target gene activity, can be introduced into cells via gene therapy methods. Alternatively, when

the target gene encodes an extracellular protein, it may be preferable to co-administer normal target gene protein into the cell or tissue to maintain the requisite level of cellular or tissue target gene activity. By contrast, in the case of oncogene-like target genes, for example, SPHK1, EDG4, EDG5, or EDG8, it is the respective normal wild type SPHK1, EDG4, EDG5, or EDG8 gene and its protein that need to be suppressed. Thus, any mutant or variants that are defective in SPHK1, EDG4, EDG5, or EDG8 function or that interferes or completely abolishes its normal function would be desirable for cancer treatment. Therefore, the same methodologies described above to safeguard normal gene alleles may be used in the present invention to safeguard the mutants of the target gene in the application of antisense, ribozyme, and triple helix treatment.

Anti-sense RNA and DNA or DNA decoy, ribozyme, and triple helix molecules of the invention can be prepared by standard methods known in the art for the synthesis of DNA and RNA molecules. These include techniques for chemically synthesizing oligodeoxyribonucleotides and oligoribonucleotides well known in the art, for example, solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules can be generated by *in vitro* and *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences can be incorporated into a wide variety of vectors which also include suitable RNA polymerase promoters, for example, the T7 or SP6 polymerase promoters. Alternatively, antisense cDNA constructs that synthesize antisense RNA constitutively or inducibly, depending on the promoter used, can be introduced stably into cell lines. Various well-known modifications to the DNA molecules can be introduced as a means for increasing intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences of ribo- or deoxy- nucleotides to the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

In this aspect, the present invention also provides negative modulatory techniques using antibodies. Antibodies can be generated which are both specific for a target gene product and which reduce target gene product activity; they can be administered when negative modulatory techniques are appropriate for the treatment of tumors and cancers, for example, in the case of

SPHK1, EDG4, EDG5, or EDG8 antibodies for colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, or bladder cancer treatment.

In instances where the target gene protein to which the antibody is directed is intracellular, and whole antibodies are used, internalizing antibodies are preferred. However, lipofectin or liposomes can be used to deliver the antibody, or a fragment of the Fab region which binds to the target gene epitope, into cells. Where fragments of an antibody are used, the smallest inhibitory fragment which specifically binds to the binding domain of the protein is preferred. For example, peptides having an amino acid sequence corresponding to the domain of the variable region of the antibody that specifically binds to the target gene protein can be used. Such peptides can be synthesized chemically or produced by recombinant DNA technology using methods well known in the art (for example, see Creighton, 1983, *supra*; and Sambrook *et al.*, 1989, *supra*). Alternatively, single chain neutralizing antibodies that bind to intracellular target gene product epitopes also can be administered. Such single chain antibodies can be administered, for example, by expressing nucleotide sequences encoding single-chain antibodies within the target cell population by using, for example, techniques, for example, those described in Marasco *et al.*, *Proc. Natl. Acad. Sci. USA*, 90:7889-7893 (1993). When the target gene protein is extracellular, or is a transmembrane protein, any of the administration techniques known in the art which are appropriate for peptide administration can be used to effectively administer inhibitory target gene antibodies to their site of action. The methods of administration and pharmaceutical preparations are discussed below.

H. Cancer Vaccines Using SPHK1, EDG4, EDG5, and EDG8:

One aspect of the invention relates to methods for inducing an immunological response in a mammal which comprises inoculating the mammal with SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 polypeptide, or a fragment thereof, adequate to produce antibody and/or T cell immune response to protect the mammal from cancers, including colon cancer, ovarian cancer,

brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, or bladder cancer.

In another aspect, the invention relates to peptides derived from the SPHK1, EDG4, EDG5, or EDG8 amino acid sequence (see, for example, SEQ ID NO:2, SEQ ID NO:5, SEQ ID NO:7, or SEQ ID NO:9) where those skilled in the art would be aware that the peptides of the present invention, or analogs thereof, can be synthesized by automated instruments sold by a variety of manufacturers, can be commercially custom ordered and prepared, or can be expressed from suitable expression vectors as described above. The term amino acid analogs has been previously described in the specification and for purposes of describing peptides of the present invention, analogs can further include branched or non-linear peptides.

The present invention therefore provides pharmaceutical compositions comprising SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 proteins or peptides derived therefrom for use in vaccines and in immunotherapy methods. When used as vaccines to protect mammals against cancer, the pharmaceutical composition can comprise as an immunogen cell lysate from cells transfected with a recombinant expression vector or a culture supernatant containing the expressed protein. Alternatively, the immunogen is a partially or substantially purified recombinant protein or a synthetic peptide.

Vaccination can be conducted by conventional methods. For example, the immunogen can be used in a suitable diluent such as saline or water, or complete or incomplete adjuvants. Further, the immunogen may or may not be bound to a carrier to make the protein immunogenic. Examples of such carrier molecules include but are not limited to bovine serum albumin (BSA), keyhole limpet hemocyanin (KLH), tetanus toxoid, and the like. The immunogen can be administered by any route appropriate for antibody production such as intravenous, intraperitoneal, intramuscular, subcutaneous, and the like. The immunogen may be administered once or at periodic intervals until a significant titer of anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 antibody is produced. The antibody may be detected in the serum using an immunoassay.

In another aspect, the present invention provides pharmaceutical compositions comprising nucleic acid sequence capable of directing host organism synthesis of a SPHK1, an EDG4, an EDG5, or an EDG8 protein or of a peptide derived from the SPHK1, EDG4, EDG5, or EDG8 protein sequence. Such nucleic acid sequence may be inserted into a suitable expression vector by methods known to those skilled in the art. Expression vectors suitable for producing high efficiency gene transfer *in vivo* include, but are not limited to, retroviral, adenoviral and vaccinia viral vectors. Operational elements of such expression vectors are disclosed previously in the present specification and are known to one skilled in the art. Such expression vectors can be administered, for example, intravenously, intramuscularly, subcutaneously, intraperitoneally or orally.

Another aspect of the invention relates to methods for inducing an immunological response in a mammal which comprises inoculating the mammal with naked SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 nucleic acids, or a fragment thereof, adequate to produce an immunogenic polypeptide, which in turn would induce antibodies and/or a T cell immune response to protect the mammal from cancers, including colon cancer, ovarian cancer, brain cancer, breast cancer, lung cancer, liver cancer, kidney cancer, head and neck cancer, stomach cancer, esophagus cancer, or bladder cancer.

Naked SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 nucleic acids, as described herein, can be administered as a vaccine via various routes, including, intramuscular, intravenous, intraperitoneal, intranasal (via mucosa), intradermal, subcutaneous (see, for example, Fynan *et al. Proc Natl Acad Sci USA* 90:11478-11482 (1993); Molling K., *J Mol Med* 75:242-246 (1997)). For example, naked DNA, when injected intramuscularly, is taken up by cells, transcribed into mRNA, and expressed as protein. This protein is the actual vaccine, and it is produced by the vaccine recipient, which gives a higher chance of natural modifications and correct folding. It is presented to the immune system and induces both humoral and cellular immune responses (see, for example, Tang *et al. Nature* 356:152-154 (1992); Molling K., *J Mol Med* 75:242-246 (1997)).

According to the invention, liposome encapsulated SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 nucleic acids also can be administered. For example, clinical trials or other research studies with liposome encapsulated DNA in treating melanoma illustrated that the approach is effective in gene therapy (see, for example, Nabel, J. G., *et al.*, "Direct gene transfer with DNA-liposome complexes in melanoma: Expression, biological activity and lack of toxicity in humans", *Proc. Nat. Acad. Sci. U.S.A.*, 90:11307-11311 (1993)).

Whether the immunogen is a SPHK1, an EDG4, an EDG5, or an EDG8 protein, a peptide derived therefrom or a nucleic acid sequence capable of directing host organism synthesis of SPHK1, EDG4, EDG5, or EDG8 protein or peptides derived therefrom, the immunogen may be administered for either a prophylactic or therapeutic purposes. Such prophylactic use may be appropriate for, for example, individuals with a genetic predisposition to a particular cancer. When provided prophylactically, the immunogen is provided in advance of the cancer or any symptom due to the cancer. The prophylactic administration of the immunogen serves to prevent or attenuate any subsequent onset of cancer. When provided therapeutically, the immunogen is provided at, or shortly after, the onset of cancer or any symptom associated with the cancer.

The present invention further relates to a vaccine for immunizing a mammal, for example, humans, against cancer comprising SPHK1, EDG4, EDG5, or EDG8 protein or an expression vector capable of directing host organism synthesis of SPHK1, EDG4, EDG5, or EDG8 protein in a pharmaceutically acceptable carrier.

In addition to use as vaccines and in immunotherapy, the above compositions can be used to prepare antibodies to SPHK1, EDG4, EDG5, or EDG8 protein. To prepare antibodies, a host animal is immunized using the SPHK1, EDG4, EDG5, or EDG8 protein or peptides derived therefrom or aforementioned expression vectors capable of expressing SPHK1, EDG4, EDG5, or EDG8 protein or peptides derived therefrom. The host serum or plasma is collected following an appropriate time interval to provide a composition comprising antibodies reactive with the virus particle. The gamma globulin fraction or the IgG antibodies can be obtained, for example, by use of saturated ammonium sulfate or DEAE Sephadex, or other techniques known to those

skilled in the art. The antibodies are substantially free of many of the adverse side effects which may be associated with other drugs.

The antibody compositions can be made even more compatible with the host system by minimizing potential adverse immune system responses. This is accomplished by removing all or a portion of the Fc portion of a foreign species antibody or using an antibody of the same species as the host animal, for example, the use of antibodies from human/human hybridomas. Humanized antibodies (*i.e.*, nonimmunogenic in a human) may be produced, for example, by replacing an immunogenic portion of a non-human antibody with a corresponding, but nonimmunogenic portion (*i.e.*, chimeric antibodies). Such chimeric antibodies may contain the reactive or antigen binding portion of an antibody from one species and the Fc portion of an antibody (nonimmunogenic) from a different species. Examples of chimeric antibodies, include but are not limited to, non-human mammal-human chimeras, such as rodent-human chimeras, murine-human and rat-human chimeras (Cabilly *et al.*, *Proc. Natl. Acad. Sci. USA*, 84:3439, 1987; Nishimura *et al.*, *Cancer Res.*, 47:999, 1987; Wood *et al.*, *Nature*, 314:446, 1985; Shaw *et al.*, *J. Natl. Cancer Inst.*, 80:15553, 1988). General reviews of "humanized" chimeric antibodies are provided by Morrison S., *Science*, 229:1202, 1985 and by Oi *et al.*, *BioTechniques*, 4:214, 1986.

Alternatively, anti-SPHK1 and/or anti-EDG4 and/or anti-EDG5 and/or anti-EDG8 antibodies can be induced by administering anti-idiotypic antibodies as immunogen. Conveniently, a purified anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 antibody preparation prepared as described above is used to induce anti-idiotypic antibody in a host animal. The composition is administered to the host animal in a suitable diluent. Following administration, usually repeated administration, the host produces anti-idiotypic antibody. To eliminate an immunogenic response to the Fc region, antibodies produced by the same species as the host animal can be used or the Fc region of the administered antibodies can be removed. Following induction of anti-idiotypic antibody in the host animal, serum or plasma is removed to provide an antibody composition. The composition can be purified as described above for anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 antibodies, or by affinity chromatography

using anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 antibodies bound to the affinity matrix. The anti-idiotypic antibodies produced are similar in conformation to the authentic SPHK1, EDG4, EDG5, or EDG8 antigen and may be used to prepare vaccine rather than using a SPHK1, an EDG4, an EDG5, or an EDG8 protein.

5 To induce anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 antibodies in an animal, the method of administering the SPHK1, EDG4, EDG5, or EDG8 antigen can be the same as used in the case of vaccination, for example, intramuscularly, intraperitoneally, subcutaneously or the like in an effective concentration in a physiologically suitable diluent with or without adjuvant. One or more booster injections may be desirable.

10 For both *in vivo* use of antibodies to SPHK1, EDG4, EDG5, or EDG8 proteins and anti-idiotypic antibodies and for diagnostic use, it may be preferable to use monoclonal antibodies. Monoclonal anti-SPHK1, anti-EDG4, anti-EDG5, or anti-EDG8 antibodies, or anti-idiotypic antibodies can be produced by methods known to those skilled in the art. (Goding, J. W. 1983. *Monoclonal Antibodies: Principles and Practice*, Pladermic Press, Inc., New York, NY, pp. 56-
15 97). To produce a human-human hybridoma, a human lymphocyte donor is selected. A donor known to have the SPHK1, EDG4, EDG5, or EDG8 antigen may serve as a suitable lymphocyte donor. Lymphocytes can be isolated from a peripheral blood sample or spleen cells may be used if the donor is subject to splenectomy. Epstein-Barr virus (EBV) can be used to immortalize human lymphocytes or a human fusion partner can be used to produce human-human
20 hybridomas. Primary *in vitro* immunization with peptides also can be used in the generation of human monoclonal antibodies.

I. Pharmaceutical Applications of Compounds:

25 The identified compounds that inhibit the expression, synthesis, and/or activity of the target gene, for example, SPHK1 and/or EDG4 and/or EDG5 and/or EDG8 can be administered to a patient at therapeutically effective doses to prevent, treat, or control a tumor or cancer. A

therapeutically effective dose refers to an amount of the compound that is sufficient to result in a measurable reduction or elimination of cancer or its symptoms.

Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, for example, for determining the LD₅₀ (the dose lethal to 50% of the population) and the ED₅₀ (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and can be expressed as the ratio, LD₅₀/ED₅₀. Compounds that exhibit large therapeutic indices are preferred. While compounds that exhibit toxic side effects can be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue to minimize potential damage to normal cells and, thereby, reduce side effects.

The data obtained from the cell culture assays and animal studies can be used to formulate a dosage range for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED₅₀ with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the IC₅₀ (the concentration of the test compound that achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma can be measured, for example, by high performance liquid chromatography (HPLC).

Pharmaceutical compositions for use in the present invention can be formulated by standard techniques using one or more physiologically acceptable carriers or excipients. The compounds and their physiologically acceptable salts and solvates can be formulated and administered, for example, orally, intraorally, rectally, parenterally, epicutaneously, topically, transdermally, subcutaneously, intramuscularly, intranasally, sublingually, intradurally, intraocularly, intraspiratorally, intravenously, intraperitoneally, intrathecal, mucosally, by oral inhalation, nasal inhalation, or rectal administration, for example.

For oral administration, the pharmaceutical compositions can take the form of tablets or capsules prepared by conventional means with pharmaceutically acceptable excipients, for example, binding agents, for example, pregelatinised maize starch, polyvinylpyrrolidone, or hydroxypropyl methylcellulose; fillers, for example, lactose, microcrystalline cellulose, or calcium hydrogen phosphate; lubricants, for example, magnesium stearate, talc, or silica; disintegrants, for example, potato starch or sodium starch glycolate; or wetting agents, for example, sodium lauryl sulphate. The tablets can be coated by methods well known in the art. Liquid preparations for oral administration can take the form of solutions, syrups, or suspensions, or they can be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparations can be prepared by conventional means with pharmaceutically acceptable additives, for example, suspending agents, for example, sorbitol syrup, cellulose derivatives, or hydrogenated edible fats; emulsifying agents, for example, lecithin or acacia; non-aqueous vehicles, for example, almond oil, oily esters, ethyl alcohol, or fractionated vegetable oils; and preservatives, for example, methyl or propyl-p-hydroxybenzoates or sorbic acid. The preparations also can contain buffer salts, flavoring, coloring, and/or sweetening agents as appropriate. Preparations for oral administration can be suitably formulated to give controlled release of the active compound.

For administration by inhalation, the compounds are conveniently delivered in the form of an aerosol spray presentation from pressurized packs or a nebulizer, with the use of a suitable propellant, for example, dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide, or other suitable gas. In the case of a pressurized aerosol, the dosage unit can be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, for example, gelatin for use in an inhaler or insufflator can be formulated containing a powder mix of the compound and a suitable powder base, for example, lactose or starch.

The compounds can be formulated for parenteral administration by injection, for example, by bolus injection or continuous infusion. Formulations for injection can be presented in unit dosage form, for example, in ampoules or in multi-dose containers, with an added

preservative. The compositions can take such forms as suspensions, solutions, or emulsions in oily or aqueous vehicles, and can contain formulatory agents, for example, suspending, stabilizing, and/or dispersing agents. Alternatively, the active ingredient can be in powder form for constitution with a suitable vehicle, for example, sterile pyrogen-free water, before use. The compounds also can be formulated in rectal compositions, for example, suppositories or retention enemas, for example, containing conventional suppository bases, for example, cocoa butter or other glycerides.

Furthermore, the compounds also can be formulated as a depot preparation. Such long acting formulations can be administered by implantation (for example, subcutaneously or intramuscularly) or by intramuscular injection. Thus, for example, the compounds can be formulated with suitable polymeric or hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, or as sparingly soluble derivatives, for example, as a sparingly soluble salt.

The compositions can, if desired, be presented in a pack or dispenser device which can contain one or more unit dosage forms containing the active ingredient. The pack can for example comprise metal or plastic foil, for example, a blister pack. The pack or dispenser device can be accompanied by instructions for administration.

J. Administration of siRNA/shRNA/miRNA:

The invention includes methods of administering siRNA, shRNA, and miRNA, to a patient in need thereof, wherein the siRNA, shRNA, or miRNA molecule is delivered in the form of a naked oligonucleotide or via an expression vector as described herein.

The present invention provides methods of blocking the *in vivo* expression of SPHK1, EDG4, EDG5, or EDG8 gene by administering a naked DNA or a vector containing siRNA, shRNA, or miRNA as set forth herein (see, for example, Examples XIII to XXI), which interacts with the target gene and causes post-transcriptional silencing of specific genes in cells, for

example, mammalian cells (including human cells) and in the body, for example, mammalian bodies (including humans).

The invention also provides methods for the treatment of cells *ex vivo* by administering a naked DNA or a vector according to the invention.

5 In its *in vivo* or *ex vivo* therapeutic applications, it is appropriate to administer siRNA, shRNA, or miRNAs using a viral or retroviral vector, which enters the cell by transfection or infection. In particular, as a therapeutic product according to the invention, a vector can be a defective viral vector, such as an adenovirus, or a defective retroviral vector, such as a murine retrovirus.

10 The vector used to convey the gene construct according to the invention to its target can be a retroviral vector, which will transport the recombinant construct by a borrower capsid, and insert the genetic material into the DNA of the host cell.

Techniques that use vectors, in particular viral vectors (retroviruses, adenoviruses, adeno-associated viruses), to transport genetic material to target cells can be used to introduce genetic
15 modifications into various somatic tissues, for example, colon, ovarian, brain, breast, lung, liver, kidney, or bladder cells.

The use of retroviral vectors to transport genetic material necessitates, on the one hand, carrying out the genetic construction of the recombinant retrovirus, and on the other hand having a cell system available which provides for the function of encapsidation of the genetic material to
20 be transported:

i. In a first stage, genetic engineering techniques enable the genome of a murine retrovirus, such as Moloney virus (murine retrovirus belonging to the murine leukemia virus group (Reddy *et al.*, *Science*, 214:445-450 (1981)). The retroviral genome is cloned into a plasmid vector, from which all the viral sequences coding for the structural proteins (genes: *Gag*,
25 *Env*) as well as the sequence coding for the enzymatic activities (gene: *Pol*) are then deleted. As a result, only the necessary sequences "in cis" for replication, transcription and integration are retained (sequences corresponding to the two LTR regions, encapsidation signal and primer

binding signal). The deleted genetic sequences may be replaced by non-viral genes such as the gene for resistance to neomycin (selection antibiotic for eukaryotic cells) and by the gene to be transported by the retroviral vector, for example, SPHK1, EDG4, EDG5, or EDG8 siRNA as set forth herein.

5 ii. In a second stage, the plasmid construct thereby obtained is introduced by transfection into the encapsidation cells. These cells constitutively express the *Gag*, *Pol* and *Env* viral proteins, but the RNA coding for these proteins lacks the signals needed for its encapsidation. As a result, the RNA cannot be encapsidated to enable viral particles to be formed. Only the recombinant RNA emanating from the transfected retroviral construction is equipped with the
10 encapsidation signal and is encapsidated. The retroviral particles produced by this system contain all the elements needed for the infection of the target cells (such as CD34+ cells) and for the permanent integration of the gene of interest into these cells, for example, SPHK1, EDG4, EDG5, or EDG8 siRNA as set forth herein. The absence of the *Gag*, *Pol* and *Env* genes prevents the system from continuing to propagate.

15 DNA viruses such as adenoviruses also can be suited to this approach although, in this case, maintenance of the DNA in the episomal state in the form of an autonomous replicon is the most likely situation.

 Adenoviruses possess some advantageous properties. In particular, they have a fairly broad host range, are capable of infecting quiescent cells and do not integrate into the genome of
20 the infected cell. For these reasons, adenoviruses have already been used for the transfer of genes *in vivo*. To this end, various vectors derived from adenoviruses have been prepared, incorporating different genes (beta-gal, OTC, alpha-1At, cytokines, *etc.*). To limit the risks of multiplication and the formation of infectious particles *in vivo*, the adenoviruses used are generally modified so as to render them incapable of replication in the infected cell. Thus, the
25 adenoviruses used generally have the E1 (E1a and/or E1b) and possibly E3 regions deleted.

 The defective recombinant adenoviruses according to the invention may be prepared by any technique known to persons skilled in the art (Levrero *et al.*, *Gene*, 101:195 (1991), EP 185

573; Graham, *EMBO J.* 3:2917 (1984)). In particular, they may be prepared by homologous recombination between an adenovirus and a plasmid in a suitable cell line.

According to the present invention, an exogenous DNA sequence, for example, SPHK1, EDG4, EDG5, or EDG8 siRNA as set forth herein, is inserted into the genome of the defective recombinant adenovirus.

Pharmaceutical compositions comprising one or more viral vectors, such as defective recombinants as described above, may be formulated for the purpose of topical, oral, parenteral, intranasal, intravenous, intramuscular, subcutaneous, intraocular, and the like, administration. Preferably, these compositions contain vehicles which are pharmaceutically acceptable for an administrable formulation. These can be, in particular, isotonic, sterile saline solutions (of monosodium or disodium phosphate, sodium, potassium, calcium or magnesium chloride, and the like, or mixtures of such salts), or dry, in particular lyophilized, compositions which, on addition, as appropriate, of sterilized water or of physiological saline, enable particular injectable solutions to be made up.

The doses of defective recombinant virus used for the injection may be adapted in accordance with various parameters, and in particular in accordance with the mode of administration used, the pathology in question, the gene to be expressed or the desired duration of treatment. Generally speaking, the recombinant adenoviruses according to the invention may be formulated and administered in the form of doses of between 10^4 and 10^{14} pfu/ml, and preferably 10^6 to 10^{10} pfu/ml. The term pfu ("plaque forming unit") corresponds to the infectious power of a solution of virus, and is determined by infection of a suitable cell culture and measurement, generally after 48 hours, of the number of plaques of infected cells. The techniques of determination of the pfu titer of a viral solution are well documented in the literature.

The use of genetically modified viruses as a shuttle system for transporting the modified genetic material not only permits the genetic material to enter the recipient cell by the expedient of using a borrower viral capsid, but also allows a large number of cells to be treated

simultaneously and over a short period of time, which permits therapeutic treatment applied to the whole body.

The invention is further described by the following examples, which do not limit the invention in any manner.

EXAMPLES:

Example I: Amplification of the SPHK1 Gene in Human Cancers:

DNA microarray-based comparative genomic hybridization (CGH) was used to survey the genome for gene amplification, and it was determined that the SPHK1 gene is frequently amplified in tumor tissue and cell lines.

Genomic DNAs were isolated from colon, ovarian, brain, breast, lung, and bladder cancer samples. DNAs were analyzed, along with (i) a SPHK1 TaqMan probe representing the target and (ii) a reference probe representing a normal non-amplified, single copy region in the genome, with a TaqMan 7700 Sequence Detector (Applied Biosystems) following the manufacturer's protocol.

SPHK1 was found to be amplified in 20% (5/24) of breast cancer cell lines and 17% (15/88) of primary breast tumors. SPHK1 also was found amplified in 21% (4/19) of ovarian tumors, 33% (3/9) of bladder tumors, 6% (2/35) of colon tumors, and 3% (1/30) lung tumors (see Table 1). Cancer-free normal tissues from the above-identified source types were used as controls.

Only samples with the SPHK1 gene copy number greater than or equal to 3.0-fold are deemed to have been amplified because of current instrumental detection limit. However, an increase in SPHK1 gene copy number less than 3.0-fold can still be considered as an amplification of the gene, if detected.

Table 1. Amplification of SPHK1 in human tumors.

Tumor type	Frequency of genomic amplification*	
	Cell line	Primary tumor
Breast	20% (5/24)	17% (15/88)
Ovarian	10% (1/10)	21% (4/19)
Colon	8% (3/35)	6% (2/35)
Bladder	6% (1/17)	33% (3/9)
Lung	ND	3% (1/30)
Cervical	0% (0/9)	ND
Lymphoma	0% (0/7)	ND
Sarcoma	0% (0/7)	ND
Melanoma	11% (2/19)	ND
Brain	19% (3/16)	ND

*Amplification cutoff: 3.0X.

Example II: Overexpression of the SPHK1 mRNA in Cancer:

5 Reverse transcriptase (RT)-directed quantitative PCR was performed using the TaqMan 7700 Sequence Detector (Applied Biosystems) to determine the SPHK1 mRNA level in each sample. Human β -actin mRNA was used as control.

Total RNA was isolated from tumor samples using Trizol Reagent (Invitrogen) and treated with DNAase (Ambion) to eliminate genomic DNA. The reverse transcriptase reaction
 10 (at 48°C for 30 minutes, for example) was coupled with quantitative PCR measurement of cDNA copy number in a one-tube format according to the manufacturer (Perkin Elmer/Applied Biosystems). The nucleotide sequences of SPHK1 were used to design and make a suitable TaqMan probe set (see GenBank Accession No. NM_021972) for SPHK1. SPHK1 expression levels in the samples were normalized using human β -actin and overexpression fold was
 15 calculated by comparing SPHK1 expression in tumor v. normal samples.

The RT-TaqMan showed that SPHK1 mRNA is overexpressed in 30% (4/12) of breast cancer cell lines and 31% (17/54) of primary breast tumors. Cancer-free normal tissues from the above-identified source types were used as controls. A good correlation is observed between

amplification and overexpression of SPHK1 in the same tumor sample or cell line tested (see Table 2). However, overexpression of SPHK1 mRNA also has been observed at fairly high levels in the absence of gene amplification (see, for example, Sample ID 9182 in Table 2). Similar phenomenon also has been noted with other genes (see, for example, Yoshimoto *et al.*,
 5 *JPN J. Cancer Res.*, 77(6):540-5, 1986).

Table 2: Correlation between SPHK1 Amplification and Overexpression.

Sample ID	Amplification*	Expression*
AlaB	5.6	4
MDAMB361	4.3	5.4
ZR75-1	10.5	6.2
MDAMB134	1.6	8.2
8772	5	5.1
9031	5.1	6.5
10571	3.5	5.5
10623	3	5.7
8896	1.2	27
9182	0.8	>100
10627	1.3	8.8

* Relative fold of genomic amplification and mRNA expression were measured by TaqMan and RT- TaqMan.

Example III: Physical Map of the Amplicon Containing the SPHK1 Gene Locus:

Cancer cell lines or primary tumors are examined for DNA copy number of genes and markers near SPHK1 to map the boundaries of the amplified regions.

DNA is purified from tumor cell lines or primary tumors. The DNA copy number of
 15 each marker in each sample is directly measured using PCR and a fluorescence-labeled probe. The number of PCR cycles needed to cross a preset threshold, also known as Ct value, in the

sample tumor DNA preparations and a series of normal human DNA preparations at various concentrations is measured for both the target probe and a known single-copy DNA probe using Applied Biosystems 7700 TaqMan machine. The relative abundance of target sequence to the single-copy probe in each sample is then calculated by statistical analyses of the Ct values of the unknown samples and the standard curve is generated from the normal human DNA preparations at various concentrations.

To determine the DNA copy number for each of the genes, corresponding probes to each marker are designed using PrimerExpress 1.0 (Applied Biosystems) and synthesized by Operon Technologies. Subsequently, the target probe (representing the marker), a reference probe (representing a normal non-amplified, single copy region in the genome), and tumor genomic DNA (10 ng) are subjected to analysis by the Applied Biosystems 7700 TaqMan Sequence Detector following the manufacturer's protocol.

Example IV: Amplification of the EDG4 Gene in Human Tumors:

DNA microarray-based comparative genomic hybridization (CGH) was used to survey the genome for gene amplification, and it was determined that the EDG4 gene is frequently amplified in tumor tissues.

Genomic DNAs were isolated from breast, colon, lung, ovarian, liver, stomach, head and neck, esophagus, or kidney cancer samples. DNAs were analyzed, along with (i) an EDG4 TaqMan probe representing the target and (ii) a reference probe representing a normal non-amplified, single copy region in the genome, with a TaqMan 7700 Sequence Detector (Applied Biosystems) following the manufacturer's protocol.

EDG4 was found to be amplified and/or overexpressed in human breast, colon, lung, ovarian, liver, stomach, head and neck, esophagus, or kidney tumors (see Figures 1 and 2). More specifically, EDG4 was found to be amplified in over 10% (6/58) of human breast tumors, over 11% (11/99) of human colon tumors, over 25% (20/78) of human lung tumors, 6% (2/34) of human ovarian tumors, over 17% (6/35) of human head and neck tumors, over 13% (5/38) of

human liver tumors, 29% (15/52) of human kidney tumors, over 22% (8/36) of human stomach tumors, and 12% (5/42) of human esophagus tumors (see Figure 1). Cancer-free normal tissues from the above-identified source types were used as controls.

Only samples with the EDG4 gene copy number greater than or equal to 3.0-fold are deemed to have been amplified because of current instrumental detection limit. However, an increase in EDG4 gene copy number less than 3.0-fold can still be considered as an amplification of the gene, if detected.

Example V: Overexpression of the EDG4 mRNA in Tumors:

Reverse transcriptase (RT)-directed quantitative PCR was performed using the TaqMan 7700 Sequence Detector (Applied Biosystems) to determine the EDG4 mRNA level in each sample. Human β -actin mRNA was used as control.

Total RNA was isolated from tumor samples using Trizol Reagent (Invitrogen) and treated with DNAase (Ambion) to eliminate genomic DNA. The reverse transcriptase reaction (at 48°C for 30 minutes, for example) was coupled with quantitative PCR measurement of cDNA copy number in a one-tube format according to the manufacturer (Perkin Elmer/Applied Biosystems). The nucleotide sequences of EDG4 were used to design and make a suitable TaqMan probe set (see GenBank Accession No. NM_004720) for EDG4. EDG4 expression levels in the samples were normalized using human β -actin and overexpression fold was calculated by comparing EDG4 expression in tumor v. normal samples.

The RT-TaqMan showed that EDG4 mRNA is overexpressed in breast, colon, lung, ovarian, head and neck, liver, and kidney tumors (see Figure 2). More specifically, EDG4 was found to be overexpressed in over 12% (6/47) of human breast tumors, over 17% (6/35) of human colon tumors, over 1% (1/78) of human lung tumors, over 19% (6/31) of human ovarian tumors, over 3% (1/28) of human head and neck tumors, 26% (8/31) of human liver tumors, and over 22% (7/31) of human kidney tumors (see Figure 2). Cancer-free normal tissues from the above-identified source types were used as controls.

The folds of amplification and folds of overexpression were measured by TaqMan and RT-TaqMan, respectively, using EDG4-specific fluorogenic TaqMan probes.

A good correlation is observed between amplification and overexpression of EDG4 in the same tumor samples tested (see Table 3).

EDG4 was initially identified by microarray analysis of breast tumor 144A1 (at chromosome 19p12). A follow-up screening by quantitative PCR revealed that EDG4 is amplified and/or overexpressed in breast and other tumors. A good correlation between EDG4-gene amplification and overexpression was observed (see Table 3).

Table 3: Correlation between EDG4 Amplification and Overexpression.*

Tumor Samples	Amplification	Overexpression
<i>Breast</i>		
144A1	4.3	15.08
<i>Colon</i>		
86-528	5.3	4.8
<i>Lung</i>		
LUTU12	6.8	4.32
<i>Ovarian</i>		
CHTN 544	4.6	4.53
<i>Liver</i>		
1158A1	14.6	6.16
1592A1	5.7	4.67
2067A1	2.9	6.32
<i>Kidney</i>		
7476B1	4.4	5.03
7464B1	3	9.68
7468B1	5.4	5.45
7483B1	5.3	13.16
7454B1	3.5	6.33

* Relative fold of genomic amplification and mRNA expression were measured by TaqMan and RT- TaqMan.

Example VI: Physical Map of the Amplicon Containing the EDG4 Gene Locus:

Cancer cell lines or primary tumors were examined for DNA copy number of genes and markers near EDG4 to map the boundaries of the amplified regions.

DNA was purified from tumor cell lines or primary tumors. The DNA copy number of each marker in each sample was directly measured using PCR and a fluorescence-labeled probe. The number of PCR cycles needed to cross a preset threshold, also known as Ct value, in the sample tumor DNA preparations and a series of normal human DNA preparations at various concentrations was determined for both the target probe and a known single-copy DNA probe using a TaqMan 7700 Sequence Detector (Applied Biosystems). The relative abundance of target sequence to the single-copy probe in each sample was then calculated by statistical analyses of the Ct values of the unknown samples and the standard curve was generated from the normal human DNA preparations at various concentrations.

To determine the DNA copy number for each of the genes, corresponding probes to each marker were designed using PrimerExpress 1.0 (Applied Biosystems) and synthesized by Operon Technologies. Subsequently, the target probe (representing the marker), a reference probe (representing a normal non-amplified, single copy region in the genome), and tumor genomic DNA (10 ng) were subjected to analysis by the TaqMan 7700 Sequence Detector (Applied Biosystems) following the manufacturer's protocol. The epicenter mapping around EDG4 gene was performed using amplified tumor and tumor cell line samples. Referring to Figure 3, the EDG4 gene is indicated by an arrow. The amplified tumor samples used include 86-528, LUTU12, 106-192-0058, 144A1, 7476B1, 7464B1, 7468B1, 7483B1, and 7454B1. The number of DNA copies for each sample was plotted against genomic distance according to UCSC genome browser (<http://genome.ucsc.edu>) in Figure 3. The number of DNA copies for each sample is plotted on the Y-axis, and the X-axis corresponds to nucleotide position based on Human Genome Project working draft sequence (<http://genome.ucsc.edu/goldenPath/aug2001Tracks.html>). Figure 3 shows epicenter mapping of 19p12 amplicon, which includes the EDG4 locus. A full-length EDG4 gene was present at the epicenter.

Example VII: Amplification of the EDG5 Gene in Human Tumors:

DNA microarray-based comparative genomic hybridization (CGH) was used to survey the genome for gene amplification, and it was determined that the EDG5 gene is frequently amplified in tumor tissues.

Genomic DNAs were isolated from colon, breast, lung, liver, and bladder tumor cells. DNAs were analyzed, along with (i) an EDG5 TaqMan probe representing the target and (ii) a reference probe representing a normal non-amplified, single copy region in the genome, with a TaqMan 7700 Sequence Detector (Applied Biosystems) following the manufacturer's protocol.

Overall, EDG5 was found to be amplified in 20% of human lung tumors, 21% of human breast tumors, 23% of human colon tumors, 10% of human liver tumors, and over 22% of human bladder tumors (see Table 4). Cancer-free normal tissues from the above-identified source types were used as controls.

Only samples with the EDG5 gene copy number greater than or equal to 3.0-fold are deemed to have been amplified because of current instrumental detection limit. However, an increase in EDG5 gene copy number less than 3.0-fold can still be considered as an amplification of the gene, if detected.

Table 4. Amplification and overexpression of EDG5 in human tumors.

Tumor type	Amplification*		Co-amplification with EDG8	Overexpression	
	Frequency (No. per No. of samples tested)	Maximum Fold		Frequency (No. per No. of samples tested)	Maximum Fold
Lung	20% (8/40)	5X to 8X	88% (7/8)	Not done	Not done
Breast	21% (21/100)	5X to 13X	67% (14/21)	32% (6/19)	6X to 11X
Colon	23% (8/35)	5X to 21X	75% (6/8)	45% (17/38)	5X to 100X
Liver	10% (2/19)	5X to 10X	100% (2/2)	Not done	Not done
Bladder	22% (2/9)	5X to 15X	100% (2/2)	Not done	Not done

* Amplification cutoff: 3.0X.

Example VIII: Overexpression of the EDG5 mRNA in Tumors:

Reverse transcriptase (RT)-directed quantitative PCR was performed using the TaqMan 7700 Sequence Detector (Applied Biosystems) to determine the EDG5 mRNA level in each sample. Human β -actin mRNA was used as control.

Total RNA was isolated from tumor samples using Trizol Reagent (Invitrogen) and treated with DNAase (Ambion) to eliminate genomic DNA. The reverse transcriptase reaction (at 48°C for 30 minutes, for example) was coupled with quantitative PCR measurement of cDNA copy number in a one-tube format according to the manufacturer (Perkin Elmer/Applied Biosystems). The nucleotide sequences of EDG5 were used to design and make a suitable TaqMan probe set (see GenBank Accession No. NM_004230) for EDG5. EDG5 expression levels in the samples were normalized using human β -actin and overexpression fold was calculated by comparing EDG5 expression in tumor v. normal samples.

The RT-TaqMan showed that EDG5 mRNA is overexpressed in colon, breast, lung, liver, and bladder tumors. More specifically, the overexpression of EDG5 was found in 32% (6/19) of breast tumors and 45% (17/38) of colon tumors tested (see Table 4). Cancer-free normal tissues from the above-identified source types were used as controls. A good correlation is observed between amplification and overexpression of EDG5 in the same tumor samples tested (see Table 4).

Example IX: Physical Map of the Amplicon Containing the EDG5 Gene Locus:

Cancer cell lines or primary tumors were examined for DNA copy number of genes and markers near EDG5 to map the boundaries of the amplified regions.

DNA was purified from tumor cell lines or primary tumors. The DNA copy number of each marker in each sample was directly measured using PCR and a fluorescence-labeled probe. The number of PCR cycles needed to cross a preset threshold, also known as Ct value, in the sample tumor DNA preparations and a series of normal human DNA preparations at various

concentrations was determined for both the target probe and a known single-copy DNA probe using a TaqMan 7700 Sequence Detector (Applied Biosystems). The relative abundance of target sequence to the single-copy probe in each sample was then calculated by statistical analyses of the Ct values of the unknown samples and the standard curve was generated from the normal human DNA preparations at various concentrations.

To determine the DNA copy number for each of the genes, corresponding probes to each marker were designed using PrimerExpress 1.0 (Applied Biosystems) and synthesized by Operon Technologies. Subsequently, the target probe (representing the marker), a reference probe (representing a normal non-amplified, single copy region in the genome), and tumor genomic DNA (10 ng) were subjected to analysis by the TaqMan 7700 Sequence Detector (Applied Biosystems) following the manufacturer's protocol. The epicenter mapping around EDG5 gene was performed using amplified tumor and tumor cell line samples. Referring to Figure 4, the EDG5 gene is indicated by an arrow. The amplified tumor samples used include CHTN875, CHTN883, CHTN885, CHTN890, CHTN894, 88-682, 88-249, 97-145, 90-794, and 90-594. The number of DNA copies for each sample was plotted against genomic distance according to UCSC genome browser (<http://genome.ucsc.edu>) in Figure 4. The number of DNA copies for each sample is plotted on the Y-axis, and the X-axis corresponds to nucleotide position based on Human Genome Project working draft sequence (<http://genome.ucsc.edu/goldenPath/avg2001Tracks.html>). Figure 4 shows epicenter mapping of 19p13.3 amplicon, which includes the EDG5 locus. A full-length EDG5 gene was present at the epicenter.

Example X: Amplification of the EDG8 Gene in Cancer:

DNA microarray-based comparative genomic hybridization (CGH) was used to survey the genome for gene amplification, and it was determined that the EDG8 gene is frequently amplified in tumor tissues and cell lines.

Genomic DNAs were isolated from colon, breast, lung, liver, and bladder tumor cells. DNAs were analyzed, along with (i) an EDG8 TaqMan probe representing the target and (ii) a

reference probe representing a normal non-amplified, single copy region in the genome, with a TaqMan 7700 Sequence Detector (Applied Biosystems) following the manufacturer's protocol.

EDG8 was found to be amplified in 17% of human lung tumors, 10% of human breast tumors, 26% of human colon tumors, 10% of human liver tumors, and over 22% of human
 5 bladder tumors (Table 5). Cancer-free normal tissues from the above-identified source types were used as controls.

Table 5: DNA amplification and overexpression of EDG8 in human tumors.

Tumor type	Amplification*		Overexpression**	
	Frequency (No. per No. of samples tested)	Maximum Fold	Frequency (No. per No. of samples tested)	Maximum Fold
Lung	17% (5/30)	5X to 11X	32% (6/19)	5X to 26X
Breast	10% (10/100)	3X to 20X	74% (14/19)	5X to 21X
Colon	26% (9/35)	3X to 27X	68% (13/19)	5X to >100X
Liver	10% (2/19)	3X to 4X	Not done	Not done
Bladder	22% (2/9)	5X to 9X	Not done	Not done

*Amplification cutoff: 3.0X.

**Relative to expression levels in corresponding normal tissue.

10 Only samples with the EDG8 gene copy number greater than or equal to 3.0-fold are deemed to have been amplified because of current instrumental detection limit. However, an increase in EDG8 gene copy number less than 3.0-fold can still be considered as an amplification of the gene, if detected.

Example XI: Overexpression of the EDG8 mRNA in Tumors:

Reverse transcriptase (RT)-directed quantitative PCR was performed using the TaqMan 7700 Sequence Detector (Applied Biosystems) to determine the EDG8 mRNA level in each sample. Human β -actin mRNA was used as control.

Total RNA was isolated from tumor samples using Trizol Reagent (Invitrogen) and treated with DNAase (Ambion) to eliminate genomic DNA. The reverse transcriptase reaction (at 48°C for 30 minutes, for example) was coupled with quantitative PCR measurement of cDNA copy number in a one-tube format according to the manufacturer (Perkin Elmer/Applied Biosystems). The nucleotide sequences of EDG8 were used to design and make a suitable TaqMan probe set (see GenBank Accession No. NM_030760) for EDG8. EDG8 expression levels in the samples were normalized using human β -actin and overexpression fold was calculated by comparing EDG8 expression in tumor v. normal samples.

The RT-TaqMan showed that EDG8 mRNA is overexpressed in colon, breast, lung, liver, and bladder tumors. More specifically, the overexpression of EDG8 was found in 32% (6/19) of lung tumors, 74% (14/19) of breast tumors, and 68% (13/19) of colon tumors tested (see Table 5). A good correlation is observed between amplification and overexpression of EDG8 in the same tumor samples tested (see Table 5). Cancer-free normal tissues from the above-identified source types were used as controls.

EDG8 was initially identified by microarray analysis of colon cancer cell line LS1034 (at chromosome 19p13). A follow-up screening by quantitative PCR revealed that EDG8 is amplified and/or overexpressed in colon and other tumors. A good correlation between EDG8-gene amplification and overexpression was observed (see Table 6).

EDG5 and EDG8 genes are found co-amplified in 67%-100% of the various types of tumor samples tested (see Table 4).

Table 6: Correlation between EDG8 Amplification and Overexpression.

Tumor sample	Amplification	Overexpression
<i>Colon Tumor</i>		
chtn872	5	57
chtn873	4.4	22
chtn874	3.4	>100
chtn875	12	20
chtn879	4.7	17
chtn885	13	>100
chtn888	3.7	30
chtn890	10	9
chtn891	5	52
chtn894	19	>100
<i>Breast Tumor</i>		
95-377	3.4	5.4
96-109	8.8	11
95-347	6.1	6.5

Example XII: Physical Map of the Amplicon Containing the EDG8 Gene Locus:

Cancer cell lines or primary tumors were examined for DNA copy number of genes and
5 markers near EDG8 to map the boundaries of the amplified regions.

DNA was purified from tumor cell lines or primary tumors. The DNA copy number of
each marker in each sample was directly measured using PCR and a fluorescence-labeled probe.
The number of PCR cycles needed to cross a preset threshold, also known as Ct value, in the
sample tumor DNA preparations and a series of normal human DNA preparations at various
10 concentrations was determined for both the target probe and a known single-copy DNA probe
using a TaqMan 7700 Sequence Detector (Applied Biosystems). The relative abundance of
target sequence to the single-copy probe in each sample was then calculated by statistical

analyses of the Ct values of the unknown samples and the standard curve was generated from the normal human DNA preparations at various concentrations.

To determine the DNA copy number for each of the genes, corresponding probes to each marker were designed using PrimerExpress 1.0 (Applied Biosystems) and synthesized by Operon Technologies. Subsequently, the target probe (representing the marker), a reference probe (representing a normal non-amplified, single copy region in the genome), and tumor genomic DNA (10 ng) were subjected to analysis by the TaqMan 7700 Sequence Detector (Applied Biosystems) following the manufacturer's protocol. The epicenter mapping around EDG8 gene was performed using amplified tumor and tumor cell line samples. Referring to Figure 4, the EDG8 gene is indicated by an arrow. The amplified tumor samples used include CHTN875, CHTN883, CHTN885, CHTN890, CHTN894, 88-682, 88-249, 97-145, 90-794, and 90-594. The number of DNA copies for each sample was plotted against genomic distance according to UCSC genome browser (<http://genome.ucsc.edu>) in Figure 4. The number of DNA copies for each sample is plotted on the Y-axis, and the X-axis corresponds to nucleotide position based on Human Genome Project working draft sequence (<http://genome.ucsc.edu/goldenPath/avg2001Tracks.html>). Figure 4 shows epicenter mapping of 19p13.3 amplicon, which includes the EDG8 locus. A full-length EDG8 gene was present at the epicenter. EDG5 is located about 100 kilo bases away from EDG8 in Chromosome 19p13.3.

Example XIII: Small Interfering RNA (siRNA):

Sense and antisense siRNAs duplexes are made based upon targeted region of a DNA sequence SPHK1, EDG4, EDG5, or EDG8 sequences, as disclosed herein (see, for example, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, or a fragment thereof), are typically less than 100 base pairs ("bps") in length and constituency and preferably are about 30 bps or shorter, and are made by approaches known in the art, including the use of complementary DNA strands or synthetic approaches. SiRNA derivatives employing polynucleic acid modification techniques, such as peptide nucleic acids, also can be employed according to the invention. The siRNAs are capable of causing interference and can cause post-

transcriptional silencing of specific genes in cells, for example, mammalian cells (including human cells) and in the body, for example, mammalian bodies (including humans). Exemplary siRNAs according to the invention have up to 30 bps, 29 bps, 25 bps, 22 bps, 21 bps, 20 bps, 15 bps, 10 bps, 5 bps or any integer thereabout or therebetween.

5 A targeted region is selected from the DNA sequence (for example, SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, or a fragment thereof). Various strategies are followed in selecting target regions and designing siRNA oligos, for example, 5' or 3' UTRs and regions nearby the start codon should be avoided, as these may be richer in regulatory protein binding sites. Designed sequences preferably include AA-(N27 or
10 less nucleotides)-TT and with about 30% to 70% G/C-content. If no suitable sequences are found, the fragment size is extended to sequences AA(N29 nucleotides). The sequence of the sense siRNA corresponds to, for example, (N27 nucleotides)-TT or N29 nucleotides, respectively. In the latter case, the 3' end of the sense siRNA is converted to TT. The rationale for this sequence conversion is to generate a symmetric duplex with respect to the sequence
15 composition of the sense and antisense 3' overhangs. It is believed that symmetric 3' overhangs help to ensure that the small interfering ribonucleoprotein particles (siRNPs) are formed with approximately equal ratios of sense and antisense target RNA-cleaving siRNPs (Elbashir *et al. Genes and Dev.* 15:188-200, 2001).

20 **Example XIV: SPHK1 siRNA:**

Sense or antisense siRNAs are designed based upon targeted regions of a DNA sequence, as disclosed herein (see, for example, SEQ ID NO:3, GenBank Accession No. NM_021972), and include fragments having up to 30 bps, 29 bps, 25 bps, 22 bps, 21 bps, 20 bps, 15 bps, 10 bps, 5 bps or any integer thereabout or therebetween. For example, 19 bps siRNA include:

25 Targeted region (base position numbers 12-30, SEQ ID NO:11)

5'-GGTCGGTTGCGGACGTGGC-3',

the corresponding sense siRNA (SEQ ID NO:12), and

5'- GGUCGGUUGCGGACGUGGC-3';

Targeted region (base position numbers 72-90, SEQ ID NO:13)

5'-GCTCCCGCGGCCCTGCCGC-3', and

the corresponding sense siRNA (SEQ ID NO:14)

5 5'-GCUCCCGCGGCCCUGCCGC-3';

Targeted region (base position numbers 123-141, SEQ ID NO:15)

5'-GGGCAAGGCCTTGCAGCTC-3', and

the corresponding sense siRNA (SEQ ID NO:16)

5'-GGGCAAGGCCUUGCAGCUC-3';

10 Targeted region (base position numbers 216-234, SEQ ID NO:17)

5'-CCACGCGCGGGAGCTGGTG-3', and

the corresponding sense siRNA (SEQ ID NO:18)

5'-CCACGCGCGGGAGCUGGUG-3';

Targeted region (base position numbers 351-369, SEQ ID NO:19)

15 5'-GCCCCTGTGTAGCCTCCCA-3', and

the corresponding sense siRNA (SEQ ID NO:20)

5'- GCCCCUGUGUAGCCUCCCA-3'; and continuing in this progression to the end of
SPHK1-coding sequence, for example,

Targeted region (base position numbers 1173-1191, SEQ ID NO:21)

20 5'-GCCACCGCCAGAAGAGCCC-3', and

the corresponding sense siRNA (SEQ ID NO:22)

5'-GCCACCGCCAGAAGAGCCC-3'; and so on as set forth herein.

A set of siRNAs/shRNAs are designed based on SPHK1-coding sequence (see SEQ ID NO:3).

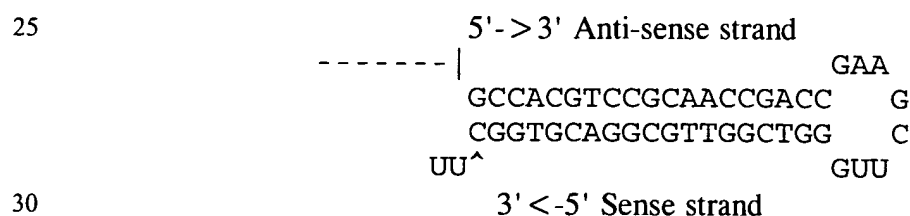
Example XV: A PCR-based Strategy for Cloning SPHK1 siRNA/shRNA

Sequences:

SPHK1 oligos can be designed based on a set criteria, for example, 19 bps 'sense' sequences (for example, a target region starting base position number 12 of the SPHK1 sequence in SEQ ID NO:3) containing a 'C' at the 3' end are selected from the SPHK1 sequence (see SEQ ID NO:11). A termination sequence (for example, AAAAAA, SEQ ID NO:23), a SPHK1 antisense sequence, a loop (for example, GAAGCTTG, SEQ ID NO:24), and a reverse primer (for example, U6 reverse primer, GGTGTTTCGTCCTTCCACAA, SEQ ID NO:25) are subsequently added to the 19 bps sense strands to construct PCR primers (Paddison *et al.*, *Genes and Dev.* 16: 948-958, 2002). Of course, other sense and anti-sense sequences can be selected from a target molecule to develop siRNAs for that molecule.

Several steps are followed in generating hairpin primers. First, a 19 nt "sense" sequence containing a "C" at the 3' end is selected. Second, the actual hairpin is constructed in a 5'-3' orientation with respect to the intended transcript. Third, a few stem pairings are changed to G-U by altering the sense strand sequence. G-U base pairing seems to be beneficial for stability of short hairpins in bacteria and does not interfere with silencing. Finally, the hairpin construct is converted to its "reverse complement" and combined with 21 nt human U6 promoter. See below, an example of the model structure drawn:

A Model shRNA structure based on SEQ ID NO:11 (5'-GGTCGGTTGCGGACGTGGC-3') is (SEQ ID NO:26):



The linear form of the model (SEQ ID NO:27):

Anti-sense **Loop** **Sense** **Termination**

5' GCCACGTCCGCAACCGACCGAAGCTTGGGTCGGTTGCGGACGTGGCTTTTTT

Some base pairing are changed to G-U by altering sense sequence. The final hairpin is converted to its reverse complement.

10 Hairpin portion of the primer (about 52 nt): (SEQ ID NO:28)

AAAAAAGCCACGTCCGCAACCGACCCAAGCTTCGGTCGGTTGCGGACGTGGC

+

U6 promoter (reverse primer sequence): GGT GTT TCG TCC TTT CCA CAA (SEQ ID NO:25)

15

Thus, the final hairpin sequence (SEQ ID NO:29) is:

AAAAAAGCCACGTCCGCAACCGACCCAAGCTTCGGTCGGTTGCGGACGTGGC
GGTGTTCGTCCTTTCCACAA

PCR and Cloning: A pGEM1 plasmid (Promega) containing the human U6 locus (G. Hannon, CSHL) is used as the template for the PCR reaction. This vector contains about 500bp of upstream U6 promoter sequence. Since an SP6 sequence flanks the upstream portion of the U6 promoter, an SP6 oligo is used as the universal primer in U6-hairpin PCR reactions. The PCR product is about 600bp in length. T-A and directional topoisomerase-mediated cloning kits (Invitrogen, Inc. Catalog No. K2040-10, K2400-20) are used according to the manufacturer's instruction.

To obtain stable SPHK1 siRNAs/shRNAs, some nucleotide bases are modified, therefore, the designed oligo sequences may not match the actual coding sequences.

Examples of oligos designed and the targeted base position numbers of the 19 nt sense sequence of the SPHK1-coding region (see, for example, SEQ ID NO:3, GenBank Accession No. NM_021972) are shown below:

5 SEQ ID NO:30: Primer containing a target region (starting base position number 12 of the SPHK1-coding sequence):

AAAAAAGCCACGTCCGCAACCGACCCAAGCTTCGGTCGGTTGCGGACGTGGC
GGTGTTCGTCCTTTCCACAA-3', and

the targeted SPHK1-coding region is (coding region base position numbers 12-30, SEQ ID NO:11) 5'-GGTCGGTTGCGGACGTGGC-3';

10 SEQ ID NO:31: Primer containing a target region (starting base position number 72 of the SPHK1-coding sequence):

AAAAAAGCGGCAGGGCCGCGGGAGCCAAGCTTCGCTCCCGCGGCCCTGCCG
CGGTGTTCGTCCTTTCCACAA-3', and

15 the targeted SPHK1-coding region is (coding region base position numbers 72-90, SEQ ID NO:12) 5'-GCTCCCGCGGCCCTGCCGC-3';

SEQ ID NO:32: Primer containing a target region (starting base position number 123 of the SPHK1-coding sequence):

AAAAAAGAGCTGCAAGGCCTTGCCCCAAGCTTCGGGCAAGGCCTTGCAGCTC
GGTGTTCGTCCTTTCCACAA-3', and

20 the targeted SPHK1-coding region is (coding region base position numbers 123-141, SEQ ID NO:33) 5'-GGGCAAGGCCTTGCAGCTC-3';

SEQ ID NO:34: Primer containing a target region (starting base position number 216 of the SPHK1-coding sequence):

25 AAAAAACACCAGCTCCCGCGCGTGGCAAGCTTCCCACGCGCGGGAGCTGGTG
GGTGTTCGTCCTTTCCACAA-3', and

the targeted SPHK1-coding region is (coding region base position numbers 216-234, SEQ ID NO:35) 5'-CCACGCGCGGGAGCTGGTG-3';

SEQ ID NO:36: Primer containing a target region (starting base position number 351 of the SPHK1-coding sequence):

5 AAAAAATGGGAGGCTACTCTGGGGCCAAGCTTCGCCCCTGTGTAGCCTCCCA
GGTGTTCGTCCTTTCCACAA-3', and

the targeted SPHK1-coding region is (coding region base position numbers 351-369, SEQ ID NO:37) 5'-GCCCCTGTGTAGCCTCCCA-3'; and

10 SEQ ID NO:38: Primer containing a target region (starting base position number 1173 of the SPHK1-coding sequence):

AAAAAAGGGCTCTTCTGGCGGTGGCCAAGCTTCGCCACCGCCAGAAGAGCCC
GGTGTTCGTCCTTTCCACAA-3', and

the targeted SPHK1-coding region is (coding region base position numbers 1173-1191, SEQ ID NO:39) 5'-GCCACCGCCAGAAGAGCCC-3'.

15

Example XVI: EDG4 siRNA:

Sense or antisense siRNAs are designed based upon targeted regions of a DNA sequence, as disclosed herein (see, for example, SEQ ID NO:4, GenBank Accession No. NM_004720), and include fragments having up to 30 bps, 29 bps, 25 bps, 22 bps, 21 bps, 20 bps, 15 bps, 10 bps, 5
20 bps or any integer thereabout or therebetween. For example, 29 bps siRNA include:

Targeted region (base position numbers 14-42, SEQ ID NO:40)

5'-GCCAGTGCTACTACAACGAGACCATCGGC-3',

the corresponding sense siRNA (SEQ ID NO:41), and

5'-GCCAGUGCUACUACAACGAGACCAUCGGC-3';

25 Targeted region (base position numbers 61-89, SEQ ID NO:42)

5'-GGCAAAGAGCTCAGCTCCCACTGGCGGCC-3', and

the corresponding sense siRNA (SEQ ID NO:43)

5'-GGCAAAGAGCUCAGCUCCCACUGGCGGCC-3';

Targeted region (base position numbers 136-164, SEQ ID NO:44)

5 5'-GTGCTGCTGACCAATCTGCTGGTCATAGC-3', and

the corresponding sense siRNA (SEQ ID NO:45)

5'-GUGCUGCUGACCAAUCUGCUGGUCAUAGC-3';

Targeted region (base position numbers 308-336, SEQ ID NO:46)

5'-GCTGGTTCCTGCGGCAGGGCTTGCTGGAC-3', and

10 the corresponding sense siRNA (SEQ ID NO:47)

5'-GCUGGUUCCUGCGGCAGGGCUUGCUGGAC-3'; and continuing in this
progression to the end of EDG4-coding sequence, for example,

Targeted region (base position numbers 1023-1051, SEQ ID NO:48)

5'-GAACGGCCACCCACTGATGGACTCCACCC-3', and

15 the corresponding sense siRNA (SEQ ID NO:49)

5'-GAACGGCCACCCACUGAUGGACUCCACCC-3'; and so on as set forth herein.

A set of siRNAs/shRNAs are designed based on EDG4-coding sequence (see SEQ ID
NO:4).

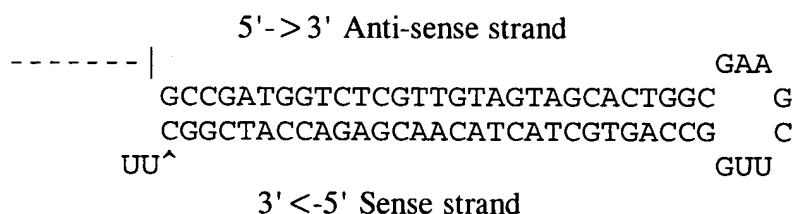
20 **Example XVII: A PCR-based Strategy for Cloning EDG4 siRNA/shRNA
Sequences:**

EDG4 oligos can be designed based on a set criteria, for example, 29 bps 'sense'
sequences (for example, a target region starting base position number 14 of the EDG4 sequence
in SEQ ID NO:4) containing a 'C' at the 3' end are selected from the EDG4 sequence (see SEQ

ID NO:40). A termination sequence (for example, AAAAAA, SEQ ID NO:23), an EDG4 antisense sequence, a loop (for example, GAAGCTTG, SEQ ID NO:24), and a reverse primer (for example, U6 reverse primer, GGTGTTTCGTCCTTTCCACAA, SEQ ID NO:25) are subsequently added to the 29 bps sense strands to construct PCR primers (Paddison *et al.*, *Genes and Dev.* 16: 948-958, 2002). Of course, other sense and anti-sense sequences can be selected from a target molecule to develop siRNAs for that molecule.

Several steps are followed in generating hairpin primers. First, a 29 nt "sense" sequence containing a "C" at the 3' end is selected. Second, the actual hairpin is constructed in a 5'-3' orientation with respect to the intended transcript. Third, a few stem pairings are changed to G-U by altering the sense strand sequence. G-U base pairing seems to be beneficial for stability of short hairpins in bacteria and does not interfere with silencing. Finally, the hairpin construct is converted to its "reverse complement" and combined with 21 nt human U6 promoter. See below, an example of the model structure drawn:

A Model shRNA structure based on SEQ ID NO:40 is (SEQ ID NO:50):



The linear form of the model (SEQ ID NO:51):

Anti-sense	Loop	Sense	Termination
GCCGATGGTCTCGTTGTAGTAGCACTGGCGAAGCTTGGCCAGTGCTACTACAACGAGACCATCGGCTTTTTT			

Some base pairing are changed to G-U by altering sense sequence. The final hairpin is converted to its reverse complement.

Hairpin portion of the primer (about 72 nt): (SEQ ID NO:52)

AAAAAAGCCGATGGTCTCGTTGTAGTAGCACTGGCCAAGCTTCGCCAGTGCTACTACAACGAGACCATCGGC

+

U6 promoter (reverse primer sequence): GGT GTT TCG TCC TTT CCA CAA (SEQ ID NO:25)

Thus, the final hairpin sequence (SEQ ID NO:53) is:

AAAAAAGCCGATGGTCTCGTTGTAGTAGCACTGGCCAAGCTTCGCCAGTGCTACTACAACGAGACCATCG
GCGGTGTTTCGTCCTTTCCACAA

PCR and Cloning: A pGEM1 plasmid (Promega) containing the human U6 locus (G. Hannon, CSHL) is used as the template for the PCR reaction. This vector contains about 500bp of upstream U6 promoter sequence. Since an SP6 sequence flanks the upstream portion of the U6 promoter, an SP6 oligo is used as the universal primer in U6-hairpin PCR reactions. The PCR product is about 600bp in length. T-A and directional topoisomerase-mediated cloning kits (Invitrogen, Inc. Catalog No. K2040-10, K2400-20) are used according to the manufacturer's instruction.

To obtain stable EDG4 siRNAs/shRNAs, some nucleotide bases are modified, therefore, the designed oligo sequences may not match the actual coding sequences.

Examples of oligos designed and the targeted base position numbers of the 29 nt sense sequence of the EDG4-coding region (see, for example, SEQ ID NO:4, GenBank Accession No. NM_004720) are shown below:

SEQ ID NO:54: Primer containing a target region (starting base position number 61 of the EDG4-coding sequence):

AAAAAAGGCCGCCAGTGGGAGCTGAGCTCTTTGCCCAAGCTTCGGCAAAGAG
CTCAGCTCCCACTGGCGGCCGGTGTTCGTCCTTTCCACAA-3', and

the targeted EDG4-coding region is (coding region base position numbers 61-89, SEQ ID NO:55) 5'-GGCAAAGAGCTCAGCTCCCACTGGCGGCC-3';

SEQ ID NO:56: Primer containing a target region (starting base position number 136 of the EDG4-coding sequence):

AAAAAAGCTATGACCAGCAGATTGGTCAGCAGCACCAAGCTTCGTGCTGCTG
ACCAATCTGCTGGTCATAGCGGTGTTTCGTCCTTTCCACAA-3', and

5 the targeted EDG4-coding region is (coding region base position numbers 136-164, SEQ ID NO:57) 5'-GTGCTGCTGACCAATCTGCTGGTCATAGC-3';

SEQ ID NO:58: Primer containing a target region (starting base position number 308 of the EDG4-coding sequence):

AAAAAAGACCAGCAAGCCCTGCCGCAGGAACCAGCCAAGCTTCGCTGGTTCC
10 TGCGGCAGGGCTTGCTGGACGGTGTTTCGTCCTTTCCACAA-3', and

the targeted EDG4-coding region is (coding region base position numbers 308-336, SEQ ID NO:59) 5'-GCTGGTTCCTGCGGCAGGGCTTGCTGGAC-3'; and

SEQ ID NO:60: Primer containing a target region (starting base position number 1023 of the EDG4-coding sequence):

15 AAAAAAGGGTGGAGTCCATCAGTGGGTGGCCGTTCCAAGCTTCGAACGGCCA
CCCACTGATGGACTCCACCC GGTGTTTCGTCCTTTCCACAA-3', and

the targeted EDG4-coding region is (coding region base position numbers 1023-1051, SEQ ID NO:61) 5'-GAACGGCCACCCACTGATGGACTCCACCC-3';

20 **Example XVIII: EDG5 siRNA:**

Sense or antisense siRNAs are designed based upon targeted regions of a DNA sequence, as disclosed herein (see, for example, SEQ ID NO:6, GenBank Accession No. NM_004230), and include fragments having up to 30 bps, 29 bps, 25 bps, 22 bps, 21 bps, 20 bps, 15 bps, 10 bps, 5 bps or any integer thereabout or therebetween. For example, 29 bps siRNA include:

25 Targeted region (base position numbers 2-30, SEQ ID NO:62)

5'-TGGGCAGCTTGTACTCGGAGTACCTGAAC-3',

the corresponding sense siRNA (SEQ ID NO:63), and

5'-UGGGCAGCUUGUACUCGGAGUACCUGAAC-3';

Targeted region (base position numbers 3-31, SEQ ID NO:64)

5'-GGGCAGCTTGTACTCGGAGTACCTGAACC-3', and

the corresponding sense siRNA (SEQ ID NO:65)

5'-GGGCAGCUUGUACUCGGAGUACCUGAAC-3';

Targeted region (base position numbers 4-32, SEQ ID NO:66)

5'-GGCAGCTTGTACTCGGAGTACCTGAACCC-3', and

the corresponding sense siRNA (SEQ ID NO:67)

5'-GGCAGCUUGUACUCGGAGUACCUGAACCC-3'; and continuing in this progression to the end of EDG5-coding sequence, for example,

Targeted region (base position numbers 945-973, SEQ ID NO:68)

5'-GAGGCGGGTCGGGACCCCGGGCCACCACC-3', and

the corresponding sense siRNA (SEQ ID NO:69)

5'-GAGGCGGGUCGGGACCCCGGGCCACCACC-3'; and so on as set forth herein.

A set of siRNAs/shRNAs are designed based on EDG5-coding sequence (SEQ ID NO:6).

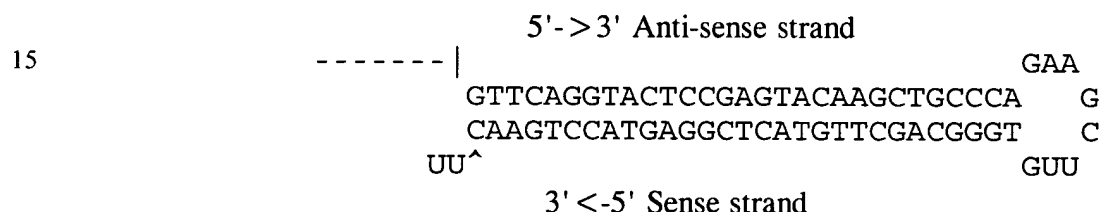
Example XIX: A PCR-based Strategy for Cloning EDG5 siRNA/shRNA Sequences:

EDG5 oligos can be designed based on a set criteria, for example, 29 bps 'sense' sequences (for example, a target region starting base position number 2 of the EDG5 sequence in SEQ ID NO:6) containing a 'C' at the 3' end are selected from the EDG5 sequence (see SEQ ID NO:62). A termination sequence (for example, AAAAAA, SEQ ID NO:23), an EDG5 antisense sequence, a loop (for example, GAAGCTTG, SEQ ID NO:24), and a reverse primer (for

example, U6 reverse primer, GGTGTTTCGTCCTTTCCACAA, SEQ ID NO:25) are subsequently added to the 29 bps sense strands to construct PCR primers (Paddison *et al.*, *Genes and Dev.* 16: 948-958, 2002). Of course, other sense and anti-sense sequences can be selected from a target molecule to develop siRNAs for that molecule.

Several steps are followed in generating hairpin primers. First, a 29 nt "sense" sequence containing a "C" at the 3' end is selected. Second, the actual hairpin is constructed in a 5'-3' orientation with respect to the intended transcript. Third, a few stem pairings are changed to G-U by altering the sense strand sequence. G-U base pairing seems to be beneficial for stability of short hairpins in bacteria and does not interfere with silencing. Finally, the hairpin construct is converted to its "reverse complement" and combined with 21 nt human U6 promoter. See below, an example of the model structure drawn:

A Model shRNA structure based on SEQ ID NO:62 is (SEQ ID NO:70):



The linear form of the model (SEQ ID NO:71):

Anti-sense	Loop	Sense	Termination
GTTCAGGTACTCCGAGTACAAGCTGCCCA	GAGCTT	TGTGGGCAGCTTGTACTCGGAGTACCTGAACTTTTTT	

Some base pairing are changed to G-U by altering sense sequence. The final hairpin is converted to its reverse complement.

Hairpin portion of the primer (about 72 nt): (SEQ ID NO:72)

AAAAAAGTTCAGGTACTCCGAGTACAAGCTGCCCAAGCTTCTGGGCAGCTTGTACTCGGAGTACCTGAAC

+

U6 promoter (reverse primer sequence): GGT GTT TCG TCC TTT CCA CAA (SEQ ID NO:25)

Thus, the final hairpin sequence (SEQ ID NO:73) is:

AAAAAAGTTCAGGTACTCCGAGTACAAGCTGCCCCACAAGCTTCTGGGCAGCTTGTACTCGGAGTACCTGAA
CGGTGTTTCGTCCTTTCCACAA

5

PCR and Cloning: A pGEM1 plasmid (Promega) containing the human U6 locus (G. Hannon, CSHL) is used as the template for the PCR reaction. This vector contains about 500bp of upstream U6 promoter sequence. Since an SP6 sequence flanks the upstream portion of the U6 promoter, an SP6 oligo is used as the universal primer in U6-hairpin PCR reactions. The PCR product is about 600bp in length. T-A and directional topoisomerase-mediated cloning kits (Invitrogen, Inc. Catalog No. K2040-10, K2400-20) are used according to the manufacturer's instruction.

To obtain stable EDG5 siRNAs/shRNAs, some nucleotide bases are modified, therefore, the designed oligo sequences may not match the actual coding sequences.

15 Examples of oligos designed and the targeted base position numbers of the 29 nt sense sequence of the EDG5-coding region (see, for example, SEQ ID NO:6, GenBank Accession No. NM_004230) are shown below:

SEQ ID NO:74: Primer containing a target region (starting base position number 3 of the EDG5-coding sequence):

20 AAAAAAGGTTCAGGTACTCCGAGTACAAGCTGCCCCAAGCTTCGGGCAGCTT
GTACTCGGAGTACCTGAACCGGTGTTTCGTCCTTTCCACAA-3', and

the targeted EDG5-coding region is (coding region base position numbers 3-31, SEQ ID NO:75) 5'-GGGCAGCTTGTACTCGGAGTACCTGAACC-3';

25 SEQ ID NO:76: Primer containing a target region (starting base position number 4 of the EDG5-coding sequence):

AAAAAAGGGTTCAGGTACTCCGAGTACAAGCGGCCCAAGCTTCGGCAGCTTG
TACTCGGAGTACCTGAACCCGGTGTTCGTCCTTTCCACAA-3', and

the targeted EDG5-coding region is (coding region base position numbers 4-32, SEQ ID NO:77) 5'-GGCAGCTTGTA CTCTCGGAGTACCTGAACCC-3'; and

SEQ ID NO:78: Primer containing a target region (starting base position number 945 of the EDG5-coding sequence):

5 AAAAAAGGTGGTGGCCCGGGGTCCCGACCCGCCTCCAAGCTTCGAGGCGGGT
CGGGACCCCGGGCCACCACCGGTGTTTCGTCCTTTCCACAA-3', and

the targeted EDG5-coding region is (coding region base position numbers 945-973, SEQ ID NO:79) 5'-GAGGCGGGTCGGGACCCCGGGCCACCACC-3'.

10 **Example XX: EDG8 siRNA:**

Sense or antisense siRNAs are designed based upon targeted regions of a DNA sequence, as disclosed herein (see, for example, SEQ ID NO:10, GenBank Accession No. NM_030760), and include fragments having up to 30 bps, 29 bps, 25 bps, 22 bps, 21 bps, 20 bps, 15 bps, 10 bps, 5 bps or any integer thereabout or therebetween. For example, 29 bps siRNA include:

15 Targeted region (base position numbers 2-30, SEQ ID NO:80)

5'-TGGAGTCGGGGCTGCTGCGGCCGGCGCCG-3',

the corresponding sense siRNA (SEQ ID NO:81), and

5'-UGGAGUCGGGGCUGCUGCGGCCGGCGCCG-3';

Targeted region (base position numbers 3-31, SEQ ID NO:82)

20 5'-GGAGUCGGGGCUGCUGCGGCCGGCGCCG-3', and

the corresponding sense siRNA (SEQ ID NO:83)

5'-GGGGAAUGGGAUGAACAAGA UCCUGCCCG-3';

Targeted region (base position numbers 4-32, SEQ ID NO:84)

5'-GAGTCGGGGCTGCTGCGGCCGGCGCCGGT-3', and

the corresponding sense siRNA (SEQ ID NO:85)

5'-GAGUCGGGGCUGCUGCGGCCGGCGCCGGU-3'; and continuing in this progression to the end of EDG8-coding sequence, for example,

Targeted region (base position numbers 1166-1194, SEQ ID NO:86)

5'-GGACTCTGGTATCAGAACCGGCTGCAGAC-3', and

the corresponding sense siRNA (SEQ ID NO:87)

5'-GGACUCUGGUAUCAGAACCGGCUGCAGAC-3'; and so on as set forth herein.

A set of siRNAs/shRNAs are designed based on EDG8-coding sequence (SEQ ID NO:10).

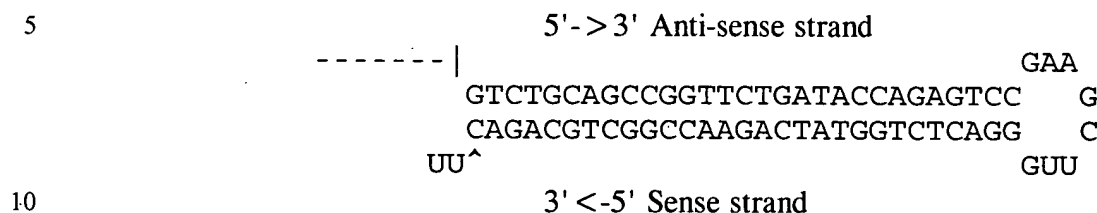
Example XXI: A PCR-based Strategy for Cloning EDG8 siRNA/shRNA Sequences:

EDG8 oligos can be designed based on a set criteria, for example, 29 bps 'sense' sequences (for example, a target region starting base position number 1166 of the EDG8 sequence in SEQ ID NO:10) containing a 'C' at the 3' end are selected from the EDG8 sequence (see SEQ ID NO:86). A termination sequence (for example, AAAAAA, SEQ ID NO:23), an EDG8 antisense sequence, a loop (for example, GAAGCTTG, SEQ ID NO:24), and a reverse primer (for example, U6 reverse primer, GGTGTTTCGTCCTTCCACAA, SEQ ID NO:25) are subsequently added to the 29 bps sense strands to construct PCR primers (Paddison *et al.*, *Genes and Dev.* 16: 948-958, 2002). Of course, other sense and anti-sense sequences can be selected from a target molecule to develop siRNAs for that molecule.

Several steps are followed in generating hairpin primers. First, a 29 nt "sense" sequence containing a "C" at the 3' end is selected. Second, the actual hairpin is constructed in a 5'-3' orientation with respect to the intended transcript. Third, a few stem pairings are changed to G-U by altering the sense strand sequence. G-U base pairing seems to be beneficial for stability of short hairpins in bacteria and does not interfere with silencing. Finally, the hairpin construct is

converted to its "reverse complement" and combined with 21 nt human U6 promoter. See below, an example of the model structure drawn:

A Model shRNA structure based on SEQ ID NO:86 is (SEQ ID NO:88):



The linear form of the model (SEQ ID NO:89):

	Anti-sense	Loop	Sense	Termination
15	GTCTGCAGCCGGTTCTGATACCAGAGTCCGAAGCTTGGGACTCTGGTATCAGAACCGGCTGCAGACTTTTTT			

Some base pairing are changed to G-U by altering sense sequence. The final hairpin is converted to its reverse complement.

20 Hairpin portion of the primer (about 72 nt): (SEQ ID NO:90)

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AAAAAAGTCTGCAGCCGGTTCTGATACCAGAGTCCCAAGCTTCGGACTCTGGTATCAGAACCGGCTGCAGAC
+
  
```

U6 promoter (reverse primer sequence): GGT GTT TCG TCC TTT CCA CAA (SEQ ID NO:25).

25 Thus, the final hairpin sequence (SEQ ID NO:91) is:

```

AAAAAAGTCTGCAGCCGGTTCTGATACCAGAGTCCCAAGCTTCGGACTCTGGTATCAGAACCGGCTGCAGA
CGGTGTTTCGTCCTTTCCACAA
  
```

30 **PCR and Cloning:** A pGEM1 plasmid (Promega) containing the human U6 locus (G. Hannon, CSHL) is used as the template for the PCR reaction. This vector contains about 500bp of upstream U6 promoter sequence. Since an SP6 sequence flanks the upstream portion of the

U6 promoter, an SP6 oligo is used as the universal primer in U6-hairpin PCR reactions. The PCR product is about 600bp in length. T-A and directional topoisomerase-mediated cloning kits (Invitrogen, Inc. Catalog No. K2040-10, K2400-20) are used according to the manufacturer's instruction.

- 5 To obtain stable EDG8 siRNAs/shRNAs, some nucleotide bases are modified, therefore, the designed oligo sequences may not match the actual coding sequences.

Examples of oligos designed and the targeted base position numbers of the 29 nt sense sequence of the EDG8-coding region (see, for example, SEQ ID NO:10, GenBank Accession No. NM_030760) are shown below:

- 10 SEQ ID NO:92: Primer containing a target region (starting base position number 20 of the EDG8-coding sequence):

AAAAAAGACGATGACCTCGCTCACCGGCGCCGGCCCAAGCTTCGGCCGGCGC
CGGTGAGCGAGGTCATCGTCGGTGTTTCGTCCTTTCCACAA-3', and

- the targeted EDG8-coding region is (coding region base position numbers 20-48, SEQ ID
15 NO:93) 5'-GGCCGGCGCCGGTGAGCGAGGTCATCGTC-3';

SEQ ID NO:94: Primer containing a target region (starting base position number 21 of the EDG8-coding sequence):

AAAAAAGGACGATGACCTCGCTCACCGGCGCCGGCCCAAGCTTCGCCGGCGCC
GGTGAGCGAGGTCATCGTCCGGTGTTTCGTCCTTTCCACAA-3', and

- 20 the targeted EDG8-coding region is (coding region base position numbers 21-49, SEQ ID NO:95) 5'-GCCGGCGCCGGTGAGCGAGGTCATCGTCC-3';

SEQ ID NO:96: Primer containing a target region (starting base position number 422 of the EDG8-coding sequence):

- AAAAAAGCGCCCCGACTGGAGACGGGCGCGGGCCCAAGCTTCGGCCCGCG
25 CCCGTCTCCAGTCGGGGGCGCGGTGTTTCGTCCTTTCCACAA-3', and

the targeted EDG8-coding region is (coding region base position numbers 422-450, SEQ ID NO:97) 5'-GGCCCGCGCCCGTCTCCAGTCGGGGGCGC-3'; and

SEQ ID NO:98: Primer containing a target region (starting base position number 1166 of the EDG8-coding sequence):

5 AAAAAAGTCTGCAGCCGGTTCTGATACCAGAGTCCCAAGCTTCGGACTCTGG
TATCAGAACCGGCTGCAGACGGTGTTCGTCCTTTCCACAA-3', and

the targeted EDG8-coding region is (coding region base position numbers 1166-1194, SEQ ID NO:99) 5'-GGACTCTGGTATCAGAACCGGCTGCAGAC-3'.

10 **Example XXII: Inhibition of S1P Activity by Anti-S1P Antibody:**

An anti-S1P antibody, as described herein, can be produced using S1P protein or a fragment thereof. An anti-S1P antibody can specifically bind a polypeptide encoded by a S1P gene or a subsequence thereof. An anti-S1P antibody can inhibit a wide spectrum of biological activities, including stimulation of cell growth, regulation of actin cytoskeleton, modulation of cell shape, cell migration, cell proliferation, modulation of cell motility. Moreover, an anti-S1P antibody can inhibit a signalling pathway that regulates diverse cellular functions, including cell growth, proliferation and survival. An anti-S1P antibody can inhibit both intracellular and extracellular functions. Intracellularly, an anti-S1P antibody can inhibit regulation proliferation and survival, and extracellularly, it can inhibit the ability of S1P to serve as a ligand for EDG family G-protein coupled receptors.

20 Anti-S1P antibodies can be used for treating cancer or precancerous growth in a mammalian tissue such as colon tissue, an ovarian tissue, a breast tissue, a lung tissue, a brain tissue, or a bladder tissue. Anti-S1P antibodies, like other antibodies herein, can be in the form of polyclonal antibodies, monoclonal antibodies, antibody fragments, single chain antibodies, humanized antibodies and synthetic antibodies from combinatorial libraries.

An effective amount of anti-S1P can be administered to a patient in need to treat a cancer such as a colon cancer, an ovarian cancer, a breast cancer, a lung cancer, a brain cancer, or a

bladder cancer. Carriers, formulations and excipients available to the skilled person can be employed with anti-S1P antibodies using known administration routes (systemic and local) and doses determined based upon the age and weight of the patient and the type and location of the cancer.

5 It is to be understood that the description, specific examples and data, while indicating exemplary embodiments, are given by way of illustration and are not intended to limit the present invention. Various changes and modifications within the present invention will become apparent to the skilled artisan from the discussion, disclosure and data contained herein, and thus are considered part of the invention.

10

SEQ ID NO:1. *Homo sapiens* sphingosine kinase 1 (SPHK1) DNA sequence (1869 bps). The GenBank Accession No. for human SPHK1 is NM_021972.

```

1  GCTCCGCGGC GCCGGCTGCG AAGTTGAGCG AAAAGTTTGA GGCCGGAGGG AGCGAGGCCG
61 GGGAGTCCGC TCCAGCGGGG CGCTCCAGTC CCTCAGACGT GGGCTGAGCT TGGGACGAGC
121 TGC GTTCCGC CCCAGGCCAC TG TAGGGAAC GGCGGTGGCG CCTCCCCAGC AAACCGGACC
181 GACTGGGTCC AGCCGCCGCA GGGAATGACA CCGGTGCTCC TACAGCCACG GCTCCGGGCG
241 GGAAGGCGA GCCCCACAGC CGGCCCTGCG ACGCCCTCCT GGCAGCACC GATAAGGAGC
301 TGAAGGCAGG AGCCGCCGCC ACGGGCAGCG CCCCCACAGC GCCAGGACC CCCTGGCAGC
361 GGGAGCCGCG GGTCGAGGTT ATGGATCCAG TGGTCGGTTG CGGACGTGGC CTCTTTGGTT
421 TTGTTTTCTC AGCGGGCGGC CCCC GGCGTGCTCCCGC GCCCTGCCGC GTGCTGGTGC
481 TGCTGAACCC GCGCGGCGGC AAGGGCAAGG CCTTGCAGCT CTTCCGAGT CACGTGCAGC
541 CCCTTTTGGC TGAGGCTGAA ATCTCCTTCA CGCTGATGCT CACTGAGCGG CGGAACCACG
601 CGCGGGAGCT GGTGCGGTCTG GAGGAGCTGG GCCGCTGGGA CGCTCTGGTG GTCATGTCTG
661 GAGACGGGCT GATGCACGAG GTGGTGAACG GGCTCATGGA GCGGCCTGAC TGGGAGACCG
721 CCATCCAGAA GCCCCTGTGT AGCCTCCAG CAGGCTCTGG CAACGCGCTG GCAGCTTCCT
781 TGAACCATTA TGCTGGCTAT GAGCAGGTCA CCAATGAAGA CCTCCTGACC AACTGCACGC
841 TATTGCTGTG CCGCCGGCTG CTGTCACCCA TGAACCTGCT GTCTCTGCAC ACGGCTTCGG
901 GGCTGCGCCT CTTCTCTGTG CTCAGCCTGG CCTGGGGCTT CATTGCTGAT GTGGACCTAG
961 AGAGTGAGAA GTATCGGCGT CTGGGGGAGA TGCCTTCAC TCTGGGCACC TTCCTGCGTC
1021 TGGCAGCCCT GCGCACCTAC CGCGGCCGAC TGGCCTACCT CCCTGTAGGA AGAGTGGGT
1081 CCAAGACACC TGCTCCCCC GTTGTGGTCC AGCAGGGCCC GGTAGATGCA CACCTTGTGC
1141 CACTGGAGGA GCCAGTGCCC TCTCACTGGA CAGTGGTGCC CGACGAGGAC TTTGTGCTAG
1201 TCCTGGCACT GCTGCACTCG CACCTGGGCA GTGAGATGTT TGCTGCACCC ATGGGCCGCT
1261 GTGCAGCTGG CGTCATGCAT CTGTTCTACG TCGGGGCGGG AGTGTCTCGT GCCATGCTGC
1321 TGCGCCTCTT CCTGGCCATG GAGAAGGGCA GGCATATGGA GTATGAATGC CCCTACTTGG
1381 TATATGTGCC CGTGGTCGCC TTCCGCTTGG AGCCCAAGGA TGGGAAAGGT GTGTTTGCAG
1441 TGGATGGGGA ATTGATGGTT AGCAGAGCCG TGCAGGGCCA GGTGCACCCA AACTACTTCT
1501 GGATGGTCAG CGGTTGCGTG GAGCCCCCGC CCAGCTGGAA GCCCCAGCAG ATGCCACCGC
1561 CAGAAGAGCC CTTATGACCC CTGGGCCGCG CTGTGCCTTA GTGTCTACTT GCAGGACCCT
1621 TCCTCCTTCC CTAGGGCTGC AGAGCCTGTC CACAGCTCCT GTGGGGGTGG AGGAGACTCC
1681 TCTGGAGAAG GGTGAGAAGG TGGAGGCTAT GCTTTGGGGG GACAGGCCAG AATGAAGTCC
1741 TGGGTCAGGA GCCCAGCTGG CTGGGCCAG CTGCCATATG AAGGCCTTCT AGTTTGTCTCT
1801 GAGACCCCA CCCCACGAAC CAAATCCAAA TAAAGTGACA TTCCCAGCCT GAAAAAAAAA
1861 AAAAAAAAAA

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SEQ ID NO:2. Human SPHK1 polypeptide sequence (398 amino acids): The GenBank Protein ID. number is NP_068807.2.

NH₂- MDPVVGCGRGLFGFVFSAGGPRGVLPRPCRVLVLLNPRGGKGKA
 LQLFRSHVQPLLAEEISFTLMLTERRNHARELVRSEELGRWDALVMSGDGLMHEVV
 NGLMERPDWETAIQKPLCSLPAGSGNALAASLNHYAGYEQVTNEDLLTNCTLLLCRRL
 LSPMNLLSLHTASGLRFLSVLSLAWGFIADVLESEKYRRLGEMRFTLGTFRLRLAALR
 TYRGRLAYLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVPDEDFVLVLA
 LLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAMLLRLFLAMEKGRHMEYECPYLV
 YVPVVAFRLEPKDGKGVFAVDGELMVSEAVQQGVHPNYFWMVSGCVEPPPSWKPQQMP
 PPEEPL -COOH

SEQ ID NO:3. *Homo sapiens* sphingosine kinase 1 (SPHK1) coding sequence (1197 bps). The GenBank Accession No. for human SPHK1 is NM_021972.

1	ATGGATCCAG	TGGTCGGTTG	CGGACGTGGC	CTCTTTGGTT	TTGTTTTCTC	AGCGGGCGGC
61	CCCCGGGGCG	TGCTCCCGCG	GCCCTGCCGC	GTGCTGGTGC	TGCTGAACCC	GCGCGGCGGC
121	AAGGGCAAGG	CCTTGCACT	CTTCCGGAGT	CACGTGCAGC	CCCTTTTGGC	TGAGGCTGAA
181	ATCTCCTTCA	CGCTGATGCT	CACTGAGCGG	CGGAACCACG	CGCGGGAGCT	GGTGCAGTGC
241	GAGGAGCTGG	GCCGCTGGGA	CGCTCTGGTG	GTCATGTCTG	GAGACGGGCT	GATGCACGAG
301	GTGGTGAACG	GGCTCATGGA	GCGGCCTGAC	TGGGAGACCG	CCATCCAGAA	GCCCCTGTGT
361	AGCCTCCCAG	CAGGCTCTGG	CAACGCGCTG	GCAGCTTCCT	TGAACCATTA	TGCTGGCTAT
421	GAGCAGGTCA	CCAATGAAGA	CCTCCTGACC	AACTGCACGC	TATTGCTGTG	CCGCCGGCTG
481	CTGTACACCA	TGAACCTGCT	GTCTCTGCAC	ACGGCTTCGG	GGCTGCGCCT	CTTCTCTGTG
541	CTCAGCCTGG	CCTGGGGCTT	CATTGCTGAT	GTGGACCTAG	AGAGTGAGAA	GTATCGGCGT
601	CTGGGGGAGA	TGCGCTTCAC	TCTGGGCACC	TTCTGCGTC	TGGCAGCCCT	GCGCACCTAC
661	CGCGGCCGAC	TGGCCTACCT	CCCTGTAGGA	AGAGTGGGTT	CCAAGACACC	TGCCTCCCCC
721	GTTGTGGTCC	AGCAGGGCCC	GGTAGATGCA	CACCTTGTGC	CACTGGAGGA	GCCAGTGCCC
781	TCTCACTGGA	CAGTGGTGCC	CGACGAGGAC	TTTGTGCTAG	TCCTGGCACT	GCTGCACTCG
841	CACCTGGGCA	GTGAGATGTT	TGCTGCACCC	ATGGGCCGCT	GTGCAGCTGG	CGTCATGCAT
901	CTGTTCTACG	TGCGGGCGGG	AGTGTCTCGT	GCCATGCTGC	TGCGCCTCTT	CCTGGCCATG
961	GAGAAGGGCA	GGCATATGGA	GTATGAATGC	CCCTACTTGG	TATATGTGCC	CGTGGTCGCC
1021	TTCCGCTTGG	AGCCCAAGGA	TGGGAAAGGT	GTGTTTGCAG	TGGATGGGGA	ATTGATGGTT
1081	AGCGAGGCCG	TGCAGGGCCA	GGTGCACCCA	AACTACTTCT	GGATGGTCAG	CGGTTGCGTG
1141	GAGCCCCCGC	CCAGCTGGAA	GCCCCAGCAG	ATGCCACCGC	CAGAAGAGCC	CTTATGA

SEQ ID NO:4. *Homo sapiens* endothelial differentiation, lysophosphatidic acid, G-protein-coupled receptor, 4 (EDG4), coding sequence (1056 bps bps). *Homo sapiens* endothelial differentiation, sphingolipid G-protein-coupled receptor, 4 (EDG4). The GenBank Accession No. for human EDG4 is NM_004720.

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1  ATGGTCATCA TGGGCCAGTG CTACTACAAC GAGACCATCG GCTTCTTCTA TAACAACAGT
61  GGCAAAGAGC TCAGCTCCCA CTGGCGGCCC AAGGATGTGG TCGTGGTGGC ACTGGGGCTG
121 ACCGTCAGCG TGCTGGTGCT GCTGACCAAT CTGCTGGTCA TAGCAGCCAT CGCCTCCAAC
181 CGCCGCTTCC ACCAGCCCAT CTACTACCTG CTCGGCAATC TGGCCGCGGC TGACCTCTTC
241 GCGGGCGTGG CCTACCTCTT CCTCATGTTC CACACTGGTC CCCGCACAGC CCGACTTTCA
301 CTTGAGGGCT GGTTCTGCG GCAGGGCTTG CTGGACACAA GCCTCACTGC GTCGGTGGCC
361 AACTGCTGG CCATCGCCGT GGAGCGGCAC CGCAGTGTGA TGGCCGTGCA GCTGCACAGC
421 CGCCTGCCCC GTGGCCGCGT GGTCATGCTC ATTGTGGGCG TGTGGGTGGC TGCCCTGGGC
481 CTGGGGCTGC TGCCTGCCCA CTCCTGGCAC TGCCTCTGTG CCCTGGACCG CTGCTCACGC
541 ATGGCACCCC TGCTCAGCCG CTCCTATTTG GCCGTCTGGG CTCTGTGCGAG CCTGCTTGTC
601 TTCCTGCTCA TGGTGGCTGT GTACACCCGC ATTTTCTTCT ACGTGCGGCG GCGAGTGCAG
661 CGCATGGCAG AGCATGTCTG CTGCCACCCC CGCTACCGAG AGACCACGCT CAGCCTGGTC
721 AAGACTGTTG TCATCATCCT GGGGGCGTTC GTGGTCTGCT GGACACCAGG CCAGGTGGTA
781 CTGCTCCTGG ATGGTTTAGG CTGTGAGTCC TGCAATGTCC TGGCTGTAGA AAAGTACTTC
841 CTACTGTTGG CCGAGGCCAA CTCACTGGTC AATGCTGCTG TGTACTCTTG CCGAGATGCT
901 GAGATGCGCC GCACCTTCCG CCGCCTTCTC TGCTGCGCGT GCCTCCGCCA GTCCACCCGC
961 GAGTCTGTCC ACTATACATC CTCTGCCAG GGAGGTGCCA GCACTCGCAT CATGCTTCCC
1021 GAGAACGGCC ACCCACTGAT GGACTCCACC CTTTAG

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SEQ ID NO:5. Human EDG4 Polypeptide Sequence (351 amino acids). The GenBank Protein ID. number is NP_004711.2.

```

NH2-
MVIMGQCYYNETIGFFYNNSGKELSSHWRPKDVVVVALGLTVSVLVLLTNLLVIAAIASNRRFHQ
PIYYLLGNLAAADLFAGVAYLFLMFHTGPRTARLSLEGWFLRQGLDTSLTASVATLLAIAVERH
RSVMAVQLHSRLPRGRVVMLIVGVVAAALGLLPAHSWHCLCALDRCSRMAPLLSRSYLAVWAL
SLLLVFLLMVAVYTRIFFYVRRRVQRMAEHVSCHPRYRETTLSLVKTVVIIIGAFVVCWTPGQVV
LLLDGLGCESC NVLAVEKYFLLLAELNSLVNAAVYSCRDAEMRRTFRRLCCACLRQSTRESVHY
TSSAQGGASTRIMLPENGHPLMDSTL -COOH

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SEQ ID NO:6. *Homo sapiens* endothelial differentiation, sphingolipid G-protein-coupled receptor, 5 (EDG5), DNA sequence. The GenBank Accession No. for human EDG5 is NM_004230.

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1 ATGGGCAGCT TGTACTCGGA GTACCTGAAC CCCAACAAGG TCCAGGAACA CTATAATTAT
61 ACCAAGGAGA CGCTGGAAAC GCAGGAGACG ACCTCCCGCC AGGTGGCCTC GGCCTTCATC
121 GTCATCCTCT GTTGCGCCAT TGTGGTGGAA AACCTTCTGG TGCTCATTGC GGTGGCCCGA
181 AACAGCAAGT TCCACTCGGC AATGTACCTG TTTCTGGGCA ACCTGGCCGC CTCCGATCTA
241 CTGGCAGGCG TGGCCTTCGT AGCCAATACC TTGCTCTCTG GCTCTGTCAC GCTGAGGCTG
301 ACGCCTGTGC AGTGGTTTGC CCGGGAGGGC TCTGCCTCCA TCACGCTCTC GGCCTCTGTC
361 TTCAGCCTCC TGGCCATCGC CATTGAGCGC CACGTGGCCA TTGCCAAGGT CAAGCTGTAT
421 GGCAGCGACA AGAGCTGCCG CATGCTTCTG CTCATCGGGG CCTCGTGGCT CATCTCGCTG
481 GTCCTCGGTG GCCTGCCCAT CCTTGGCTGG AACTGCCTGG GCCACCTCGA GGCCTGCTCC
541 ACTGTCCTGC CTCTCTACGC CAAGCATTAT GTGCTGTGCG TGGTGACCAT CTTCTCCATC
601 ATCCTGTTGG CCATCGTGGC CCTGTACGTG CGCATCTACT GCGTGGTCCG CTCAAGCCAC
661 GCTGACATGG CCGCCCCGCA GACGCTAGCC CTGCTCAAGA CGGTCACCAT CGTGCTAGGC
721 GTCTTTATCG TCTGCTGGCT GCCCGCCTTC AGCATCCTCC TTCTGGACTA TGCCTGTCCC
781 GTCCACTCCT GCCCGATCCT CTACAAAGCC CACTACTTTT TCGCCGTCTC CACCCTGAAT
841 TCCCTGCTCA ACCCGTCAT CTACACGTGG CGCAGCCGGG ACCTGCGGCG GGAGGTGCTT
901 CGGCCGCTGC AGTGCTGGCG GCCGGGGGTG GGGGTGCAAG GACGGAGGCG GGTCTGGGACC
961 CCGGGCCACC ACCTCCTGCC ACTCCGAGC TCCAGCTCCC TGGAGAGGGG CATGCACATG
1021 CCCACGTCAC CCACGTTTCT GGAGGGCAAC ACGGTGGTCT GA

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SEQ ID NO:7. Human EDG5 polypeptide sequence (353 amino acids): The GenBank Protein ID. number is NP_004221.1.

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NH2- MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFIVILC
CAIVVENLLVLIAVARNSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTP
VQWFAREGSASITLSASVFSLIAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISL
VLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRS
SHADMAAPQTLALLKTVTIVLGVFIVCWLPAFSILLLDYACPVHSCPILYKAHYFFAV
STLNSLLNPVIYTWRSRDLRREVLRLQCWRPGVGVQGRRRVGTPGHHLLPLRSSSSL
ERGMHMPTSPTFLEGNTVV -COOH

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SEQ ID NO:8. *Homo sapiens* endothelial differentiation, sphingolipid G-protein-coupled receptor, 8 (EDG8), DNA sequence. The GenBank Accession No. for human EDG8 is NM_030760.

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1  GCGCGGCCCA TGGAGTCGGG GCTGCTGCGG CCGGCGCCGG TGAGCGAGGT CATCGTCCTG
61 CATTACAACT ACACCGGCAA GCTCCGCGGT GCGCGCTACC AGCCGGGTGC CGGCCTGCGC
121 GCCGACGCCG TGGTGTGCCT GCGGTGTGTC GCCTTCATCG TGCTAGAGAA TCTAGCCGTG
181 TTGTTGGTGC TCGGACGCCA CCCGCGCTTC CACGCTCCCA TGTTCTGCT CCTGGGCAGC
241 CTCACGTTGT CGGATCTGCT GGCAGGCGCC GCCTACGCCG CCAACATCCT ACTGTCGGGG
301 CCGCTCACGC TGAAACTGTC CCCCAGCTC TGGTTCGCAC GGGAGGGAGG CGTCTTCGTG
361 GCACTCACTG CGTCCGTGCT GAGCCTCCTG GCCATCGCGC TGGAGCGCAG CCTCACCATG
421 GCGCGCAGGG GGCCCGCGCC CGTCTCCAGT CGGGGGCGCA CGCTGGCGAT GGCAGCCGCG
481 GCCTGGGGCG TGTCGCTGCT CCTCGGGCTC CTGCCAGCGC TGGGCTGGAA TTGCTGGGT
541 CGCCTGGACG CTTGCTCCAC TGTCTTGCCG CTCTACGCCA AGGCCTACGT GCTCTTCTGC
601 GTGCTCGCCT TCGTGGGCAT CCTGGCCGCG ATCTGTGCAC TCTACGCGCG CATCTACTGC
661 CAGGTACGCG CCAACGCGCG GCGCCTGCCG GCACGGCCCG GGAAGTGGGG GACCACCTCG
721 ACCCGGGGCG GTCGCAAGCC GCGCTCGCTG GCCTTGCTGC GCACGCTCAG CGTGGTGCTC
781 CTGGCCTTTG TGGCATGTTG GGGCCCCCTC TTCCTGCTGC TGTGCTCGA CGTGGCGTGC
841 CCGGCGCGCA CCTGTCTGT ACTCCTGCAG GCCGATCCCT TCCTGGGACT GGCCATGGCC
901 AACTCACTTC TGAACCCCAT CATCTACACG CTCACCAACC GCGACCTGCG CCACGCGCTC
961 CTGCGCCTGG TCTGCTGCGG ACGCCACTCC TGCGGCAGAG ACCCGAGTGG CTCCCAGCAG
1021 TCGGCGAGCG CGGCTGAGGC TTCCGGGGGC CTGCGCCGCT GCCTGCCCCC GGGCCTTGAT
1081 GGGAGCTTCA GCGGCTCGGA GCGCTCATCG CCCAGCGCG ACGGGCTGGA CACCAGCGGC
1141 TCCACAGGCA GCCCCGGTGC ACCCACAGCC GCGCGGACTC TGGTATCAGA ACCGGCTGCA
1201 GACTGACACC CTCGGCCAC GACTGTCTTC CCAAGTTTTA CAGACTTGTT CTTTTTACAT
1261 AAAGGAATTT GTAGGAAATG CAGCCAAAGG TGCAGTCGGA AAAGATGCAG GGGAAATGTA
1321 TTTATGCAGC GACACCCAC AATGTGAACA AACAGACAAA AAATCTGTGC CCTCGTGGAA
1381 TTGACGTTCT GCTTGGGAAC ACAGAAAAGA ACTCGGTGAT GAAATAATGG AGATGATTCC
1441 AGTGACAAAC GACAGAGATG GTGATGGTGG TCAGGGAAGA CCTCTCTGCA GAGGTAGTGA
1501 CTTGTGATGT GAGCTGAGAC CTCTGTCTTG GGAAGACCAA AAGAAAAGCA TTTTCAGGATG
1561 AGGGAATGGC ATGCGCAAAAG GCCCTGAGGC TGAAATGTGC CCATGTGTTC TAAGAAATGC
1621 AGCGATGCTG GTGTGCCTGG AGCAGGGACG GAGGGGGAGA ATGGGAGGAG ACAAGGAGCT
1681 GAAGGAGTAG TTCCCGAAGG ACCTTGTTGG TGATATAGAG GACTTCGCTT TTGCTCTGAG
1741 TGAGGTGGGA GCCATAGAAG CTTCTAAGCA GAAGAGGGAC TTGCCCTAAT TCAGGTGATC
1801 ACAGGTGTCT TGTGGCCTCC ATGGGAGGTT GAAAACCACA GAAGGTGAAG GGGGGCTGCA
1861 CTGAGCCACA GGAACAATGA TGGAGATTCC AGCTAAGCCC AGACCCCGTG GATTCTAGAT
1921 AGATTTTAGA GGCAGCAGAC AGAATTACTG AGGAATTGAG TGTAAGAGTG GAATAAAGTT
1981 ATCAAGGACA ATGCCAAGGG TGGGGCACCC CCAAATTTGA CTTTGGGAGA CTCAGCCAAA
2041 TCCTATCTGG TAATAAAATT TCTTTTTTAT TTTTCTTTTC TTTCTTTCTT TCTTTCTTTC
2101 TTTTTTTTTT TTTGAGTTGG GATCTTGTGC TCTGTACACC AGGCTGGAGT GCAATGGGCA
2161 CAATTATAGC TCACTGCAGC CTGGAATCC TGGGATCAAG CCTGGAGTTC CTGCTTCAGC
2221 CTCCCTAGTA GCTGGGACTA CAGGCATGCA CCACCATGCC CAGTTAATAA AATTTCTTCA
2281 AATGCAAAAA AAAAAAAAAA AAAAAA

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SEQ ID NO:9. Human EDG8 polypeptide sequence (398 amino acids): The GenBank Protein ID. number is NP_110387.1.

NH₂- MESGLLRPAPVSEVIVLHNYTGKLRGARYQPGAGLRADAVVCL
 AVCAFIVLENLAVLLVLGRHPRFHAPMFLLLGSLTSLDLLAGAAYAANILLSGPLTLK
 LSPALWFAREGGVFVALTASVLSLLAIALERSLTMARRGPAPVSSRGRTLAMAAAANG
 VSLLLGLLPALGWNCLGRLDACSTVLPLYAKAYVLCVLAFFVGILAAICALYARIYQC
 VRANARRLPARPGTAGTTSTRARRKPRSLALLRTL SVVLLAFVACWGPLFLLLLLDVA
 CPARTCPVLLQADPFLGLAMANSLLNPIIYTLTNRDLRHALLRLVCCGRHSCGRDPSG
 SQQSASAAEASGGLRRCLPPGLDGSFSGSERSSPQRDGLDTSGSTGSPGAPTAARTLV
 SEPAAD -COOH

SEQ ID NO:10. *Homo sapiens* endothelial differentiation, sphingolipid G-protein-coupled receptor, 8 (EDG8), coding sequence (1197 bps). The GenBank Accession No. for human EDG8 is NM_030760.

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1  ATGGAGTCGG GGCTGCTGCG GCCGGCGCCG GTGAGCGAGG TCATCGTCCT GCATTACAAC
61  TACACCGGCA AGCTCCGCGG TGC GCGCTAC CAGCCGGGTG CCGGCCTGCG CGCCGACGCC
121 GTGGTGTGCC TGGCGGTGTG CGCCTTCATC GTGCTAGAGA ATCTAGCCGT GTTGTGTTGGTG
181 CTCGGACGCC ACCCGCGCTT CCACGCTCCC ATGTTCTCTG TCCTGGGCAG CCTCACGTTG
241 TCGGATCTGC TGGCAGGCGC CGCCTACGCC GCCAACATCC TACTGTCGGG GCCGCTCACG
301 CTGAAACTGT CCCCCGCGCT CTGGTTCGCA CGGGAGGGAG GCGTCTTCGT GGCACCTACT
361 GCGTCCGTGC TGAGCCTCCT GGCCATCGCG CTGGAGCGCA GCCTCACCAT GGC GCGCAGG
421 GGGCCCGCGC CCGTCTCCAG TCGGGGGCGC ACGCTGGCGA TGGCAGCCGC GGCCTGGGGC
481 GTGTCGCTGC TCCTCGGGCT CCTGCCAGCG CTGGGCTGGA ATTGCCTGGG TCGCCTGGAC
541 GCTTGCTCCA CTGTCTTGCC GCTCTACGCC AAGGCCTACG TGCTCTTCTG CGTGCTCGCC
601 TTCGTGGGCA TCCTGGCCGC GATCTGTGCA CTCTACGCGC GCATCTACTG CCAGGTACGC
661 GCCAACGCGC GGCGCCTGCC GGCACGGCCC GGGACTGCGG GGACCACCTC GACCCGGGCG
721 CGTCGCAAGC CGCGCTCGCT GGCCTTGCTG CGCACGCTCA GCGTGGTGCT CCTGGCCTTT
781 GTGGCATGTT GGGGCCCCCT CTTCTGCTG CTGTTGCTCG ACGTGGCGTG CCCGGCGCGC
841 ACCTGTCTCT TACTCCTGCA GGCCGATCCC TTCCTGGGAC TGGCCATGGC CAACTCACTT
901 CTGAACCCCA TCATCTACAC GCTCACCAAC CGCGACCTGC GCCACGCGCT CCTGCGCCTG
961 GTCTGCTGCG GACGCCACTC CTGCGGCAGA GACCCGAGTG GCTCCCAGCA GTCGGCGAGC
1021 GCGGCTGAGG CTTCCGGGGG CTGCGCGCGC TGCCTGCCCC CGGGCCTTGA TGGGAGCTTC
1081 AGCGGCTCGG AGCGCTCATC GCCCCAGCGC GACGGGCTGG ACACCAGCGG CTCCACAGGC
1141 AGCCCCGGTG CACCCACAGC CGCCCGGACT CTGGTATCAG AACCGGCTGC AGACTGA
  
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